\*\*\*\*\*\*\*\*\*\*\*\* (MT)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Jun 8 21:37:37 2000; MasPar time 14.11 Seconds 692.177 Million cell updates/sec

Description:
Perfect Score:
Sequence: >US-09-316-163-9 (1-207) from US09316163.pep 1573-7 1 EDCNELPPRRNTEILTGSWS......VEISCKSPDVINGSPISQKI/207

Scoring table: PAM 150

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum\_Match 0% Lighting first 45 summaries

pir62 1:pjr1 2:pir2 3:pir3 4:pir4

Database:

Statistics: Mean 41.851; Variance 66.119; scale 0.633

pred. No. Ts the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	80	ID	Description	Pred. No.
, <sub>L</sub>	1573	100.0	449	, р	NBHUHS	factor H	0.00e+00
ω,	1154	73.4	1234	н н	NBMSH	complement factor H p	1.13e-265
4	679	43.2	669	N	S65551	bovine (f	
ហ	503	32.0	1053	N	S46199	probable complement r	6.86e-96
o	334	21.2	597	Н	S53711	C4BP alpha chain prec	6.02e-54
7	310	19.7	560	N	T16833	hypothetical protein	3.60e-48
œ	308	19.6	482	N	JC5092	E-selectin - pig	1.08e-47
9	308	19.6	830	N	A30359	P-selectin precursor	1.08e-47
10	303	19.3	2 <b>6.3</b>	1	WMVZSP	apolipoprotein H homo	1.69e-46
11	303	19.3	768	N	A42755	P-selectin precursor	1.69e-46
12	303	19.3	768	N	153821	P-selectin - rat	1.69e-46
13	297	18.9	345	ш	NBMS	apolipoprotein H prec	4.55e-45
14	298	18.9	610	N	A35046	endothelial leukocyte	2.63e-45
15	298	18.9	610	N	A32606		2,63e-45
16	292	18.6	345	۳	NBBO	apolipoprotein H prec	7.01e-44
17	293	18.6	381	μ	B26359	decay-accelerating fa	4.06e-44
18	293	18.6	440	Ν	A26359	decay-accelerating fa	4.06e-44
19	290	18.4	551	N	I46709	endothelial leukocyte	2.09e-43
20	290	18.4	597	<u>_</u>	NBHUC4	C4b-binding protein a	2.09e-43
21	288	18.3	302	ᆫ	WMBELE	secretory complement	6.22e-43
22	288	18.3	360	<u></u>	WMBE2E	membrane-bound comple	6.22e-43
23	288	18.3	612	N	S23174	endothelial leukocyte	6.22e-43

45	44	43	42	41	40	39	38	37	ω 6	ω 5	34	<u>3</u>	32	31	30	29	28	27	26	25	24
265	264	266	266	267	267	270	270	270	272	272	276	276	279	280	281	281	281	281	282	284	287
16.8	16.8	16.9	16.9	17.0	17.0	17.2	17.2	17.2	17.3	17.3	17.5	17.5	17.7	17.8	17.9	17.9	17.9	17.9	17.9	18.1	18.2
469	345	497	485	2489	2039	1091	610	345	369	362	1019	473	676	618	384	377	369	349	263	340	551
_	μ.	2	2	Ν	N	سر	۳	ш	N	N	N	N	N	N	N	Ν	Ν	2	$\vdash$	N	N
NBMSC4	JN0465	JC2054	S36772	173012	A28507	PL0009	I46001	NBHU	JC5138	JC5194	A38738	B38738	A45900	B42755	S01896	I54479	157998	G02913	C36838	I56234	146708
C4b-binding protein a	apolipoprotein H prec	complement regulatory	E-selectin - bovine	complement C3b/C4b re	complement C3b/C4b re	complement C3d/Epstei	C4b-binding protein a	apolipoprotein H prec	membrane cofactor pro	membrane cofactor pro	coagulation factor C	coagulation factor C-	complement C3b recept	E-selectin precursor	membrane cofactor pro	membrane cofactor pro	membrane cofactor pro	sperm CD46 - human (f	complement control pr	decay-accelerating fa	endothelial leukocyte
1.59e-37	2.72e-37	9.28e-38	.28e-		5.42e-38	08e-	1.08e-38	1.08e-38	3.66e-39		4.21e-40	4.21e-40	8.29e-41	4.82e-41	2.80e-41	2.80e-41	2.80e-41	2.80e-41	1.63e-41	5.49e-42	

## ALIGNMENTS

			,	1	ג או א פי ט מי
##molecule ##residues ##note	#journal #title #cross-refere #accession	##status not ##molecule_type mRNA ##residues 1-33 ##residues only REFERENCE A27877 #authors Schulz, T	# # title # toros references # accession # 600	#cross-references MUID: #accession S03013 ##molecule_type mRNA ##residues 1-44 ##cross-references E ##note part ##note ma ##note 402-	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE CACCESSIONS RECERENCE ##JOURNAL #title
	journal Eur. J. Immunol. (1986) 16:1351-1355 title Human complement factor H: isolation of cDNA clones and partial cDNA sequence of the 38-kDa tryptic fragment containing the binding site for C3b.  cross-references MUID:87054207 accession A27877	not compared with conceptual translation -type mRNA 1-33;434-449 ##label EST only portions of this 1.8 kilobase mRNA were sequenced A27877 SChulz, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Dierich, M.P.	Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. (1991) 21:799-802  Human complement factor H: two factor H proteins are derived from alternatively spliced transcripts.  nces MUID:91184292  B60238	cross-references MUID:88134059 accession \$03013 ##molecule_type mRNA ##residues 1-449 ##label RIP ##cross-references EMBL:X07523; EMBL:Y00716; NID:g32492; ##note mino:CAA30403.1; PID:g758073 ##note mature protein was confirmed by protein sequencing ##pote 402-Tyr was also found	NBHUHS #type complete complement factor H precursor, short splice form - human complement factor H-related protein; complement protein H #formal_name Homo sapiens #common_name man 31-DEC-193)#sequence_revision 23-Feb-1996 #text_change 503013; B60238; A27877; A61103; A26505; S10479 S00254 Ripoche, J.; Day_A.J.; Harris, T.J.N,; Sim, R.B. Biochem, J(1988) 249:593-602 The complete amino acid_sequence_of human complement factor

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CLASSIFICATION
                                                                                                          FEATURE
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#note the corre
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#journal J. Immunol. (1986) 136:3407-3411
Structural analysis of human complement protein H: homology
#title with C4b binding protein, beta(2)-glycoprotein I, and the
Ba fragment of B.
#cross-references MUID:86169701
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Pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.
#journal Biochemistry (1992) 31:3626-3634
#title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
#cross-references MUID:922326649
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##cross-references GB:M12383; NID:g180472; PIDN:AAA52013.1; PID:g180473
Tactor H has also been found bound to cell membranes in an unknown manner. However, it has at least one cell attachment site motif
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##molecule_type mRNA
27-76 ##label SC2
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Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in liver. See also PIR:NBHUH
                                                                                                                                                                                                                 a cofactor in the inactivation of C3b by serine proteinase I; also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway complement alternate pathway
                                                                                                                                                                                                                                                                                                                                                                    the correspondence between the two loci and the sequences indicated is unclear; factor H has been reported to have several allelic forms
                                                                                                                                          alternative splicing; complement alternate pathway;
                                                                                                                                                                                     #superfamily complement factor H; complement factor H repeat
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Sim, R.B.; DiScipio, R.G.
Biochem. J. (1982) 205:285-293
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Eur. J. Immunol. (1987) 17:1485-1489
Human complement factor H: expression of an additional truncated gene product of 43 kDa in human liver.
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                                                                                                                           glycoprotein; plasma
                    #domain signal sequence #status predicted #label SIG\
#product complement factor H, short splice form #status
experimental #label MAT\
#domain complement factor H repeat homology #label FH01\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this is a partial sequence of an alternatively spliced 1.8 kilobase mRNA that is translated to yield a 43 K form related to factor H
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Query Match
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178-205,210-251,
237-262,267-309,
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                                                                                                                                                                                                                                                                                                                                                                                                                       Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. (1991) 21:799-802
Human complement factor H: two factor H proteins are derived
Day, A.J.; Ripoche, J.; Lyons, A.; McIntosh, B.; Harris,
                                                                                                                                                                                                                                                                                                          A60238
                                                                A54726
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                                                                                              only portions of this 4.3 kilobase mRNA were sequenced
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#journal Blosci. Rep. (1986) 6:65-72
#title Partial characterization of human complement factor H by protein and cDNA sequencing: homology with other complement and non-complement proteins.
#cross-references MUID:86188123
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#title Sequence analysis of a cDNA clone encoding the C-terminal end
of human complement factor H.
#cross-references_MUID:88025472
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pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.

#journal Biochemistry (1992) 31:3626-3634

#title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.

#cross-references MUID:92232649
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#journal Biochem. J. (1982) 205:285-293
#title Purification and structural studies on the complement-system
control protein beta-1-H (factor H).
#cross-references_MUID:83048213
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##residues 'DFRN',579-1231 ##label DAY
##cross-references GB:M17517; NID:g180497; PIDN:AAA52016.1; PID:g180498
##cross-references GB:M17517; NID:g180497; PIDN:AAA52016.1; PID:g180498
##cross-references GB:M17517; NID:g180497; PIDN:AAA52016.1; PID:g180498
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##molecule_type protein
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                                                                                                                                   A.; Gordon, D.L.; Burns, G.F.
Biochim. Biophys. Acta (1996) 1289:305-311
Factor H co-purifies with thrombospondin isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Immunol. (1991) 146:3190-3196
Cloning of the 1.4-kb mRNA species of human complement factor
H reveals a novel member of the short consensus repeat
family related to the carboxy terminal of the classical
                                                                                                                                                                                                                            Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano.
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                                                           S66298
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                                                                                                                                                                                                                                                                                                                  1047-1231 ##label RES
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                          preliminary
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839-864,870-915, 901-926,931-973, 959-984,989-1032 357-385,389-431,

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##cross-references GDB:120041; OMIM:134370 #map_position 1q32-1q32 GENETICS
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#map_position 1q32-1q32
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1-66,52-80,85-129,
                 167-1228
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Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a cofactor in the inactivation of C3b by serine proteinase I; also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway complement alternate pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the correspondence between the two loci and the sequences indicated is unclear; factor H has been reported to have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alternative splicing; complement alternate pathway;
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#domain complement factor
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                                                                                                                                                                                                                                                                                                 #authors Natsuume-Sakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y.
#journal J. Immunol. (1990) 144:358-362
#title Demonstration of an unusual allelic variation of mouse factor
#toross-references MUD:90111033
#cross-references MUD:90111033
                                                          #cross-references MUID: 90148935
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1138-1163,
1167-1218,
1201-1228
217
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911
##molecule_type mRNA
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##residues 1-18 ##label RES
##cross-references GB:M31979; NID:g193726; PIDN:AAA37762.1; PID:g193729
                                                                                                                                                                                                                                                                   ##status
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                                                                                     Munoz-Canoves, P.; Tack, B.F.; Vik, D.P.
Biochemistry (1989) 28:9891-9897
Analysis of complement factor H mRNA expression:
Dexamethasone and IFN-gamma increase the level
                                           I49728
                                                                                                                                                                                                                                                                                  I49711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kristensen, T.; Tack, B.F.
Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3963-3967
Murine protein H is comprised of 20 repeating units,
acids in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Mus musculus #common_name house mouse
30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change
22-Jun-1999
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Pred. No. 0.00e+00;
0; Mismatches 0
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                                                                                                                                           Query Match 73.4%;
Best Local Similarity 68.0%;
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780-802,808-850,
836-861,867-920,
906-931,936-978,
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477-505,509-553,
536-564,569-610,
597-622,629-672,
658-683,690-732,
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114-141,146-192,

178-205,210-251,

237-862,267-309,

294-320,325-374,

357-385,389-431,
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1053-1107
1114-1168
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389-442
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##cross-references GB:J02891; NID:g193805; pIDN:AAA37795.1; PID:g553926
## Two codominant alleles of factor H are present in mice.
NT Factor H functions as a cofactor in the inactivation of C3b by
serine proteinase I and also increases the rate of dissociation
of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5
convertase) in the alternative complement pathway.
140;
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                                                                                                            Score 1154; DB 1; L
Pred. No. 1.13e-265;
33; Mismatches 33;
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                                                                                                                                                                                                                                                                                                                                                                                        FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPPVILN 126
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19_Mar-1997_#sequence_revision 25-Apr-1997 #text_change
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               Dahmen, A.; Kaidoh, T.; Zipfel, P.F.; Gigli, I.
Biochem. J. (1994) 301:391-397
Cloning and characterization of a cDNA representing
                                                                                        13-Aug-1999
S46199; S77894
                                                                                                                                                                                   probable complement regulatory plasma protein SB1 - barred
                                                                                                                              #formal_name Parablax neblifer #common_name barred sand bass
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Pred. No. 5.85e-141;
21; Mismatches 22;
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#cross-references MUID:94318039
#accession $46199
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##residues 526-532,'X',534-537;809-817,'X',819-826 ##label DAH2
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Local Similarity 41.8%;
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Blochim. Blophys. Acta (1995) 1261:285-289
Blochim. Blophys. Acta (1995) cDNA structure of rabbit C4b-binding protein alpha-chain.
Preserved sequence motive in complement regulatory protein modules which bind C4b.
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Pred. No. 6.86e-96
29; Mismatches 6
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364-422
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                                                                                                                                                                   225 VQRICLAEGIWGGNEPRCEEIRCSVLPTLPNG 256
                                                                                                                                                                                                   111 CDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGD
                                                                                                                                                                                                                                      171 CSSNGEWTNEPANCKATECSRPSSPLHGKVVGSSL-T---YQ-S-VVTYSCDHGYRLVGQ 224
                                                                                                                                                                                                                                                                                                                    117 AQWFGPD-LR-CKARACPDPGDIENG---LREGDTFEYPHHYKYSCNPGFLLYGSTS-RQ 170
                                                                                                                                                                                                                                                                                51 GEWVALNPLRKCOKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##experimental_source strain Bristol N2; clone T07H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##CIOSS-references EMBL:U53344; NID:91255886; PID:91255889.
PIDN:AAA96225.1; GSPDB:GN00028; CESP:TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **sudtus preliminary; translated from GB/EMBL/DDBJ ##molecule_type DNA ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues
                                                                                                                                                                                                                                                                                                                                                                                           Match 19.7%;
Local Similarity 33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 ISCKSPDVINGSPIS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD--GFWSKEKPKCVE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 IINGK-HNGGNE-DIH-TYGSSVTYSCNPRFSLLGEASISCTVKNKTVGVWSPSPPVCKE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 VEVKT-D-FSFGSQIEFSCSEGYILIGSTT-SHCDIQEKGVEWSDPLPKCEIVKCEPPPN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 IICSPPNVPHGKIIS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 SDQTYPEGTQAIYKCRPGYRSLG-NVIMVCR-KGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
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                                                                                                                             EEMHCSDDGFWSKEKPKCVEISCKS-PDVING 200
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E-selectin - pig
#formal_name Sus scrofa domestica #common_name domestic pig
                                   E-selectin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            14/1; 75/1; 102/3; 128/1; 186/1; 272/2; 326/1; 361/1; 422/1; 475/1; 527/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        #length 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, April 1996
The sequence of C. elegans cosmid T07H6.
T16833
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hypothetical protein T07H6.5 - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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#length 597
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#domain complement factor H repeat homology #label FH6\
#domain complement factor H repeat homology #label FH7\
#domain complement factor H repeat homology #label FH8
#th 597 #molecular-weight 66130 #checksum 6473
                                                    #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                       #molecular-weight 61619 #checksum 2418
                                                                                                                                                                                                                                                                                                                                                          Score 310; DB 2; Length 560;
Pred. No. 3.60e-48;
36; Mismatches 51; Indels 14; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 334; DB 1; Length 597; Pred. No. 6.02e-54; 37; Mismatches 72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CESP: T07H6.5
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##Cross-references GDB:120018; OMIM:173610
#map_position 1q22-1q25
CLASSIFICATION #superfamily complement factor H repeat homology;
                                                                                                                                           GENETICS
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REFERENCE
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                                                                                                                                                                                                                                                                                   #authors Johnston, G.I.; Cook, R.G.; McEver, R.P.
#journal cell (1989) 56:1033-1044
#title Cloning of GMP-140), a granule membrane protein of platelets
and endothelium: sequence similarity to proteins involved
#cross-references MUID:89168432
#accession A30359
                                                                                                                 #gene
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181-235
240-298
303-361
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                                                                                                                                        ##cross-references GB.M25322
##note parts of this sequence, including the amino end of the mature protein, were confirmed by protein sequencing
                                                                                                                                                                                                                           ##molecule_type mRNA
##residues 1-830 ##label JOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 -LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSSLEV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 NHSSIGEFAYKSTCHFTCAEGFGLQGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQPKNG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQNGDVSC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1-482 ##label WIN
##cross-references GB:U37521; NID:g1052974; PID:g1052975
This protein is a member of the selectin family of adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 TGGNVFEYGVKAV--YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 QTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 19.6%; Score 308; DB 2; Length 482;
Local Similarity 28.9%; Pred. No. 1.08e-47;
hes 52; Conservative 38; Mismatches 82; Indels
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P-selectin precursor - human
CD62 antigen; granule membrane protein 140 #
#formal_name Homo sapiens #common_name man
18 Oct-1989 #sequence_revision 30-Sep-1991 #text_change
                                                                                                            GDB:SELP; GRMP
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#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4
gth 482 #molecular-weight 52341 #checksum 7729
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200-257
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716,723,741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 GHWSAPLPTCEAISCEPLESPVHGS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 APAPVCKAVQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 GFWSKEKPKCVEISCKSPDV-INGS 201
                                                                                                                                                                                                                                                                                     ##experimental_source strain WR:NCE A42501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KCOKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 19.6%;
Local Similarity 26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                         ##residues
                                      ##molecule_type DNA
1-263 ##label GOE
                                                                                                                                                                                                                                                                                                                                                                      ##cross-references GB:X13166;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
##cross-references GB:M35027; NID:g335317; PIDN:AAA47997.1; PID:g335345
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phosphoprotein; surface antigen; transmembrane protein
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                                                                                                            Winslow, J.P.; PaoLetti, E.
Virology (1990) 179:517-563
Appendix to "The complete DNA sequence of
B42504
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apolipoprotein H homolog precursor - vaccinia virus
35K secretory protein; C3L protein; virokine
#formal_name vaccinia virus
                                                                                                                                                                                                                                                   Goebel, S.J.; Johnson, G.P.; Perkus, M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.
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Nature (1988) 335:176-178
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#domain complement factor H repeat homology #label FH02\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04\
#domain complement factor H repeat homology #label FH05\
#domain complement factor H repeat homology #label FH05\
#domain complement factor H repeat homology #label FH07\
#domain complement factor H repeat homology #label FH07\
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#domain complement factor H repeat homology #label FH08\
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#domain EGF homology #label EGF\
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#domain intracellular #status predicted #label CYT\
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Pred. No. 1.08e-47;
                                                                                                                                                                                                                                                                                                                                                                      NID:g60690; PIDN:CAA31564.1; PID:g60691
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                                                                                                                                                              vaccinia virus"
                                                                                                                                                                                                                                                                          Davis,
                                                                                                                                                                                                                                                                              S.W.;
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Best Local
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86-143
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#journal Virology (1990) 179:247-266
#title The complete DNA sequence of vaccinia virus
#cross-references MUID:91021027
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206-261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 ISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGYLCSGGE-WS-DPPTCQIVKCP 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 HPTISNG 214
                                                                                                                                                                                   ##cross-references GB:M87861; NID:g200552; PID:g200553
##experimental_source endothelial cells
                                                                                                                                                                                                                                                ##molecule_type mRNA
                                                                                                                                                                                                                                                                       ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 FILTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 LDI-GG-V-DEGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICESVKCQSPPS 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
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##status
                                                                                                                                                                     ##note
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Similarity 34.8%;
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#superfamily herpesvirus complement control protein; 
complement factor H repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD62; granule membrane protein 140; PADGEM #formal_name Mus musculus #common_name house mouse 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997
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                                                                                                                                                                                                                                                                                                                                                        Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. (1992) 267:15176-15183
Cloning of the mouse endothelial selectins. Expression of both E- and P-selectin is inducible by tumor necrosis
                                                                                                                                                                                                                                                                                             A42755
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P-selectin precursor - mouse
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                                                             Molecular cioning and analysis of in vivo expression of murine P-selectin.
                                                                                                     Sanders, W.E.; Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L. Blood (1992) 80:795-800
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                                                                                                                                                                                                                                                                         nucleic acid sequence not shown
                                                                                                                                                                   sequence extracted from NCBI backbone (NCBIP:109467)
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    nucleic acid sequence not shown
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Pred. No. 1.69e-46;
28; Mismatches 76
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163-194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398,456,467,603,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        710-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510-567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42-768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200-257
                                                                                                                                                                                                                                                                                                                                                                        y Match 19.3%;
Local Similarity 29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##Status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 EPDREYHFGQAVRFYCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV-INGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 HPIAAFAYDSSCKFECOPGYRARGSNTLHCTGSGOWSEPLPTCEAIACEPPEIPIHGS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 FSFNSQCTFSCAEGYELDGPGEL-QCLASGIWTNNPPKCDAVQCQSLEAPPHGTM-AC-M 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-723,'E',725-768 ##label SAN
##cross-references GB:M72332; NID:g193565; PID:g193566
##note sequence extracted from NCBI backbone (NCBIP:109900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAM 144
                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Auchampach, J.A.; Oliver, M.G.; Anderson, D.C.; Manning, A.M. Gene (1994) 145:251-255
Cloning, Sequence comparison and in vivo expression of the gene encoding rat P-selectin.
                                                                                                                                          #length 768
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Rattus norvegicus #common_name Norway rat 29-May-1998 #sequence_revision 29-May-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-selectin - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-Aug-1999
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#domain EGF homology #label EGF\
#domain complement factor H repeat homology #label
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#domain complement factor H repeat homology #label FH02\
#domain complement factor H repeat homology #label FH04\
#domain complement factor H repeat homology #label FH05\
#domain complement factor H repeat homology #label FH05\
#domain complement factor H repeat homology #label FH07\
#domain complement factor H repeat homology #label FH08\
#domain complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain signal sequence #status predicted #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.3%;
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                                                                                                                             #molecular-weight 83516 #checksum 4885
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intracellular #status predicted #label IMT\
   Score 303; DB 2; Le
Pred. No. 1.69e-46;
33; Mismatches 75;
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28; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 303;
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Indels 10;
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Gaps
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FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                    23-66,51-79,84-124,
110-137,142-188,
174-200,205-248,
234-260,264-315,
300-307,325-345,
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105,117,162,183,
193
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                                                                                                                                                                                                                                                                                                  142-200
205-260
                                                                                                                                                                                                                                                                                                                                                                                  84-137
                                                                                                                                                                                                                                                                      264-325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 FECOPGYRMRGSDILHCTDSGOW-S-EPLPTCEAIAC-EPLESPLHGSMDCFPSTGAFGY 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 GPLKYQSACSFSCDEGSLLVGASVIRCLATGHWSEAPPECQAVSCTP 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chylomicron; duplication; glycoprotein; HDL; heparin binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily apolipoprotein H; complement factor H repeat
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Biochem. Biophys. Res. Commun. (1994) 200:1521-1528
Characterization, expression and evolution of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B2gp1
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Molecular cloning of mouse beta-2-glycoprotein I and mapping
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apolipoprotein H precursor - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain signal sequence #status predicted #label
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#binding\_site carbohydrate (Asn) (covalent) #status

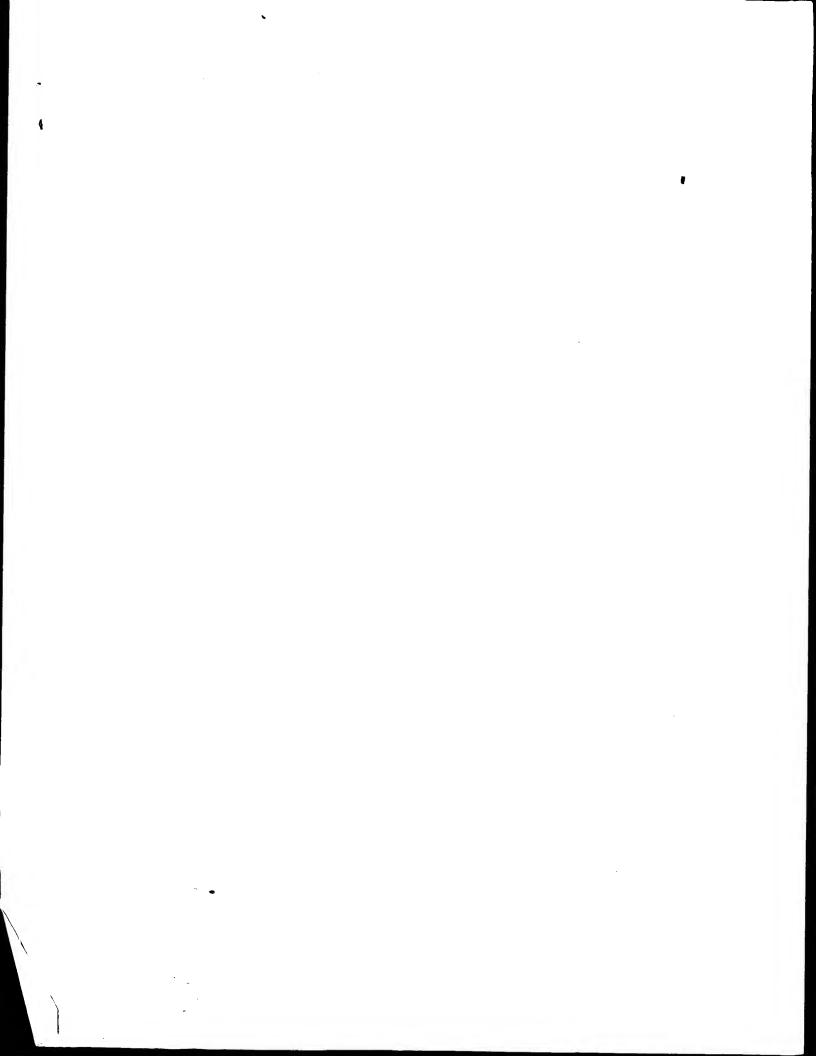
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Shows, T.; Gimbrone Jr., M.A.; Bevilacqua, M.P.

#journal J. Biol. Chem. (1991) 266:2466-2473

#title Structure and chromosomal location of the gene for
endothelial-leukocyte adhesion molecule 1.
#cross-references.MUID:91115870
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                                                                                                    210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGFVECFQNPGSFPWNTT 267
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33; Mismatches 79
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Best Local Similarity 27.4%;
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                                                                                                                                                                                                                                                           268 CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF 325
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                                                                                                                                                                                                                                                                                                                                         34 CRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFT-LTGGNVFEYGVK 91
HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bevilacqua, M.P.; Stengelin, S.; Gimbrone Jr., M.A.; Seed, I Science (1989) 243:1160-1165 Endothelial leukocyte adhesion molecule 1: an inducible receptor for neutrophils related to complement regulatory proteins and lectins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endothelial leukocyte adhesion molecule precursor - human #formal_name Homo sapiens #common_name man 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 298; DB 2; Le
Pred. No. 2.63e-45;
33; Mismatches 79;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Thu Jun 8 21:38:42 2000; MasPar time 21.93 Seconds 654.600 Million cell updates/sec

Description: Perfect Score: >US-09-316-163-9 (1-207) from US09316163.pep 1573

Sequence: 1 EDCNELPPRRNTEILIGSWS......VEISCKSPDVINGSPISQKI 207

Scoring table: PAM 150 Gap 11

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb112

"l:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_iffertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 41.889; Variance 59.758; scale 0.701

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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286	288	290	290	293	295	297	304	308	310	312	316	320	343	344	364	503	679	1573	Score
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MEMBRANE COFACTOR PROT	DJ780M13.1.1 (SELECTIN	COMPLEMENT REGULATORY	512 ANTIGEN (FRAGMENT)	ACROSOMAL MATRIX COMPO	DECAY-ACCELERATION FAC	DJ780M13.1.2 (SELECTIN	COMPLEMENT H FACTOR (F	E-SELECTIN.	COSMID T07H6.	CELL ADHESION MOLECULE	41KBP FRAGMENT FROM LE	COMPLEMENT CONTROL PRO	ORF 4.	ORF 04.	COMPLEMENT BINDING PRO	COMPLEMENT REGULATORY	CCP MODULES 3-12, WITH		Description
4.3UE-4/	1.29e-47	3.85e-48	3.85e-48	6.29e-49	1.87e-49	5.58e-50	7.96e-52	6.98e-53	2.06e-53	6.08e-54	5.28e-55	4.56e-56	3.22e-62	1.73e-62	6.97e-68	3.14e-106	4.U1e-156	0.00e+00	Pred. No.

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## ALIGNMENTS

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100.0%;	1 18 19 449 449 AA; 51033 MW;	84; sushi; 7.	CAA82763	3; AAA52U13.1; 9; AAB01987.1;	CAA30403.1;	Inmunologia.	1-9 FROM N.A.	the	1S S.A.;	1-19 FROM N.A.	136:340/-3411(198	ding protein, beta 2-glycoprotein	analysis of human	KRISTENSEN T., WETSEL R.A., TACK B.F.;	86169701.	226-449 FROM N.A.	640.000 000(+000)	"The complete amino acid sequence	J., DAY A.J., HARRIS	88134059.	M N.A.	Primates; Catarrnini;	etazoa;	(Human).	FACTOR II KEECOMOON	(TremBLrel. 12, L	01,	EMBLrel. 01,	PRELIMINARY;	
Score 1573;	POTENTIAL. POTENTIAL. 61231E1B					Hospital Trias		EMBL/GenBank/DDBJ	3			protein I, a	complement	ACK B.F.;			U	) de or	, . h .			1; HOMITHIAGE;	raniata;		•	Last annotation update)		Created)	PRT; 449	
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01-107-1996 (TremBirel. 01, Created)
01-NOV-1996 (TremBirel. 01, Last sequence update)
01-NOV-1996 (TremBirel. 12, Last annotation update)
01-NOV-1999 (TremBirel. 12, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
Paralabrax nebulifer (barred sand bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
""""""""""" Teleostei; Euteleostei; Acanthopterygii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0%; Pred. Matches 207; Conservative 0; N
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"Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b.";
Biochem. J. 315:523-531(1996).
EMBL; X98697; CAA67257.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
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Q28085;
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Local Similarity 66.18;
les 84; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQAVLPK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKGVEIFCKPPVILN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               669 AA;
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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75683 MW; FAFOD174 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 679; DB 6; Le
Pred. No. 4.01e-156;
21; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   1053 AA.
                                 Acanthopterygii; Percomorpha;
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Best Local Similarity 41.8%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9WRU2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9WRU2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem.
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[1]
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Best Local Similarity 32.6%; Pred. No. 6.97e-68; Matches 61; Conservative 40. Winner.
                                                                                                                                                                                                                                                                                                                                                                                                                                           herpesvirus 8.";
berpesvirus 8.";
J. Virol. 73:3040-3053(1999).
EMBL; AF083501; AAD21332.1; -.
EMBL; AF083501; AAD21332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 99174001.

SBARLES R.P., BERGOUAM E.P., AXTHELM M.K., WONG S.W.,

"Sequence and genomic analysis of a Rhesus macaque rhadinovirus with
similarity to Kaposi's sarcoma-associated herpesvirus/human
herpesvirus 8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TREMBLrel. 12, Last sequence update)
01-NOV-1999 (TREMBLrel. 12, Last annotation update)
COMPLEMENT BINDING PROTEIN.
Macaca mulatta rhadinovirus 17577.
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
                                                        455 ITNGKY--HPVK-DF-YQYLDTVTFSCNRDFSLVGDEMTTCISNT-WNKPFPRCEQITCS 509
                                                                                                                                                                         395 VTSGEDAFKYGTNITYKCNEGYQLLGSMYRICMLKDDLKTVDWEPKAPICDIEKCKPPPQ 454
                                                                                                                                                                                                                                                                                                 337 EKYSVGASVELICRPGFTKMQSTVSVECLSNGTWTAPNA--KCHRKKCPTPQELLNGEYI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement-regulatory plasma protein from barred sand bass (Parablax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAHMEN A., KAIDOH T., ZIPFEL P.F., GIGLI I.; "Cloning and characterization of a cDNA representing a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 SSAMEPDREYHFGQAVRFYCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN
                                                                                                                                                                                                                                        22 QTYPEGTQAIYKCRPGYRSLGNVIMV-C-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 IGG--PE-EATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PJHYDNNVQV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 EASYPGGRQVRVGCNVGY-S-GFFKLVCVEGKWETRGA--KCQPRSCGHPGDAQFADFHL 102
PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                    LTGG-NVFEYGVKAVYTCNEGYQLLGE-IN-Y--REC-DTDGWTNDIPICEVVKCLPVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 503; DB 13;
Pred. No. 3.14e-106;
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Best Local
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                        01-JAN-1998
01-JAN-1998
01-NOV-1999
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040912
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"Cell-homologous genes in the Kaposi's sarcoma-associated human herpesvirus 8: determinants of its pathogenicity?";

J. virol. 71:4187-4192(1997).

EMBL; U93872; AAB62602.1; -.

HISSP, P10998; 1VVC.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORF 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                         RUSSO J.J., BOHENZKY R.A., CHIEN M.C., CHEN J., YAN M., MADDALENA PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P88903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 97094384.
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     SEQUENCE
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                                                                                                           274:1739-1744(1996).
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 12, Last annotation update)
        550
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larity 33.9%;
Conservative
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     AA:
     60687 MW;
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                                                                                                                                                                                     WEISS R.A.,
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                                                                                                                                                            cytokine
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                                                                                                                                                                                                                                                                                             93:14862-14867(1996)
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     CEA2CAEC CRC32;
                                                                                                                                                                                     CHANG Y.;
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Best Local Similarity 37.6%;
Matches 71; Conservative
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01-MAY-1997
01-NOV-1999
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O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT CONTROL PROTEIN HOMOLOG CCPH.
                                                                                                                                                                                                                                                                                                    P87616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALBRECHT J.-C., FLECKENSTEIN B.;
"Primary Structure of the Herpesvirus Ateles Genome.";
submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF083424; AAC95530.1;
HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ateline herpesvirus 3. Viruses; dsDNA viruses,
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                                                                                                                                         Cowpox virus (CPV).
                                                                                                                                                                D17L OR C17L.
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SEQUENCE FROM N.A. STRAIN-GRI-90;
                                                                                 Orthopoxvirus.
                                                                                                                                                                                             41KBP FRAGMENT FROM LEFT
                                                                                                         Viruses; dsDNA viruses,
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Local Similarity 33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 CKSPDVING 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 CKIPQVANG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 ENGKIVSSAMEPDREYHFGQAVRFYCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-H-R-P---KIKNGDF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTGGNVFEYGVKAYYTCNEGYQLLGEINYREC -- DTDG -- - WTNDIPICEVVKCLPVTAP 134
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                                                                                                                                                                                                                     (TrEMBLrel.
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                                                                                                                                                                                          03, Created)
03, Last sequence update)
12, Last annotation update)
T END OF GENOME.
                                                                                                            no
                                                                                                            RNA stage;
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Pred. No. 3.22e-62;
38; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.56e-56; 28; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                               Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 360;
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                                                                                                               Chordopoxvirinae
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RESULT IN CONTROL OF THE PROPERTY OF THE PROPE
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Best Local S
Matches 7
     Query Match
                                                           SEQUENCE
                                                                                       CHAIN
                                                                                                                                                                                                                                                                         MANNING A.M., SANDERS W.E. JR., KUKIELKA G.L., DORE M., ROSENBLOOM C.L., HAWKINS H.L., MICHAEL L.H., ENTMAN M.L BEAUDET A.L., ANDERSON D.C.; Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases EMBL; M88170; AAA63789.1; -.
HSSP; P16109; 1FSB.
                                                                                                                SIGNAL
                                                                                                                                                                Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog).
Canis familiaris (Dog).
Curaniata; Vertebrata;
Curaniata; Vertebrata;
Curaniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TremBlrel 01, 01-NOV-1996 (TremBlrel 01, 01-NOV-1999 (TremBlrel 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q28290
Q28290;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=SPLEEN;
                                                                                                                                          NON_TER
                                                                                                                                                                                                PFAM;
                                                                                                                                                                                                                                                PROSITE; PS00615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL ADHESION MOLECULE PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins.";
Virology 243:432-460(1998).
EMBL; X94355; CAA64102.1; -.
EMBL; Y11842; CAA72567.1; -.
HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHCHELKUNOV S.N., SAFRONOV P.F., TOTMENIN A.V., PETROV N.A., RYAZANKINA O.I., GUTOROV V.V., KOTWAL G.J.; "The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 97068532.

SAFRONOV P.F., PETROV N.A., RIAZANKINA O.I., TOTMENIN A.V., SHCHELKUNOV S.N., SANDAKHCHIEV L.S.;
"Genes of a circle of hosts for the cowpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 DGFWSKEKPKCVEISCKSPDVING 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 GE-WS-DPPTCQIVKCPHPTISNG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 NPEAPICESVKCQSPPSISNGR--HNGYE-DF-YTDGSVYTYSCNSGYSLIGNSGYLCSG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 CCPIPSRPITMKFKGT-VDSHYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%;
Local Similarity 34.8%;
es 71; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                     PF00059; lectin_c; 1.
PF00084; sushi; 8.
l; Cell adhesion; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QCIKRRCPSPRDIDNGQLDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMYW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00084;
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                                                        754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sushi; 4.
                                                                                                                                                                                                                                       C_TYPE_LECTIN_1; 1.
  19.8%;
                                                        82303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28193 MW;
  Score 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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Pred. No. 5.28e-55;
30; Mismatches 84
                                                              POTENTIAL.
CELL ADHESION MOLECULE.
                                                  E9570281 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76531F63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 84; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           754 AA.
DB 6;
Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                            SMITH C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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Q22328
Q22328;
Q22328;
Q1-NOV-1996 (Tremblrel. 0
01-NOV-1996 (Tremblrel. 0
01-NOV-1999 (Tremblrel. 0
COSMID T07H6.
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BONNFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON &
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINORE B., O'CALLACHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPEA N., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U53344; AAA96225.1; -. HSSP; P10998; IVVC. PFAM; PF00084; sushi; 7. SEQUENCE 560 AA; 61619 MW; 3A10AF63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94150718
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Eukaryota; Metazoa; Nem
                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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225 VQRICLAEGIWGGNEPRCEEIRCSVLPTLPNG
                                                                                                                                                                                                                                          117 AQWFGPD-LR-CKARACPDPGDIENG---LREGDTFEYPHHVKYSCNPGFLLVGSTS-RQ 170
                                                                                                                                                                                   51 GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 PDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 SFY-CTEGYELNGPSKLECLASGTWIN-KPPR-CVATQC-PPLKTPEQGSMNCLHSVEAF 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                   CSSNGEWTNEPANCKATECSRPSSPLHGKVVGSSL-T---YQ-S-VVTYSCDHGYRLVGQ 224
                                                            CDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSRAFQYNTSCRFHCAEGFRLEGADLVQCTDLGQWTAPAPACQALQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QYQSSCHFSCEEGFALVGP-EVVQCTASGMWTAAAPVCEAVACGPLKSPVHGSMDCSp-- 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTP-FGTFT-LTGGNVF
                                                                                                                                                                                                                                                                                                          19.7%;
Similarity 33.6%;
51; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (APR-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematoda;
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12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oda; Secernentea;
Rhabditidae; Pelc
                                                                                                                                                                                                                                                                                                             Score 310; DB 5;
Pred. No. 2.06e-53;
36; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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oderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                    Length 560;
                                                                                                                                                                                                                                                                                                          Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D., SHOWNKEEN R.
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                                                                                                                                                                                                                                                                                                          Gaps
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Matches 5
        Query Match
Best Local (
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PFAM; PF000059; lectin_c; 1.
PFAM; PF00084; sushi; 4.
PRINTS; PR00043; SELECTIN.
Lectin; Glycoprotein.
SEQUENCE 482 AA; 52341 MW; 9
                                                                                                                                                    MEDLINE; 88025472.

DAY A.J., RIPOCHE J., LYONS A., MCINTOSH B., "Sequence analysis of a CDNA clone encoding thuman complement factor H.";

Biosci. Rep. 7:201-207(1987).

EMBL; M17517, AAA52-2016.1;

EMBL; M17517, PARS2016.1;

EMBL; M17517, PARS2016.1;

EMBL; M17517, PARS2016.1;
                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U37521; AAC48680.1; -.
HSSP; P16581; 1ESL.
PROSITE; PS00615; C_TYPE_LECTIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The intron-exon structure of Gene 176:67-72(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WINKLER H., BROSTJAN C., CSIZMADIA V., NATARAJAN G., ANRATHER J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E-SELECTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 -LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSSLEV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254
  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 TGGNVFEYGVKAV -- YMCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
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les 52; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQNGDVSC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
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                                                                                                                               PF00084; sushi; 11.
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                                                                           AA;
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19.3%;
27.1%;
                                                                              74247 MW;
                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
Score 304; DB 4;
Pred. No. 7.96e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 308; DB 6;
Pred. No. 6.98e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Mismatches
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                                                                           F4AB5238 CRC32;
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                                                                                                                                                                                                                                                                                 HARRIS T.J.,
                     Length
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                                                                                                                                                                                                                                                           C-terminal
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                                                                                                                                                                                                                                                              P78361 PRELIMINARY; PRT; 347 AA.
P78361;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DECAY-ACCELERATION FACTOR (FRAGMENT).
TISSUE-BRAIN HIPPOCAMPUS; KUMAR V.B., HYUNG C., NAKRA R., WALTERS M., SASSER T., Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Primates; Catarrhini; Hominida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O95508 PRELIMINARY; PRT; 740 AA.
095508;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
NON_TER 740 740
SEQUENCE 740 AA; 81390 MW; 5CEFCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AL022146; CAA18143.1; -. HSSP; P16109; 1KJD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 -VNCS-HPFGAFRY-QSVCSFTCNEGLLLVGASVLQCLATGNWNSVPPECQAIPCTP 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 AFAYGSSCKFECQPGYRVRGLDMLRCIDSGHWSA--PLPTCEAISC-EPLESPVHGSMDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 CEGLPCKSPPEISHGVVAHMSDS-YQYGEEVTYKCFEGFGIDGPAIAK-CLGEKWSHP-P 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 CSQ-PPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKW-S-SP-PQ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 TYPEGTQAIYKCRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPF-GTFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGG-NVFEYGVKAVYTCNEGYOLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCIKTDCLSLPSFENA-IPMGEKK-D-VYKAGEQVTYTCATYYKMDGASNVTCINSR-WT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAYYTCNEGYQLLGEINYRECDTDGWTNDIP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVSSAMEPDREYHFGQAV-RFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPSLRAFQYDTNCSFRCAEGFMLRGADIVR-CDNLGQWTAPAPVCQALQCQDLPVPNEAR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GRPTCRDTSCVNPPTVQNAYIVSRQM 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 297; DB 4; L
Pred. No. 5.58e-50;
39; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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                                                                                                                                                                       Hominidae;
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                                                                                                                                                                                                   Vertebrata; Mammalia;
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ORB569 PRELIMINARY; PRT; 533 AA.
ORB569;
ORB569;
ORD-JUL-1997 (TrEMBLrel. 04, Created)
ORJ-JUL-1997 (TrEMBLrel. 04, Last sequence update)
ORSOMAL MATRIX COMPONENT AM67 PRECURSOR.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLSON G.E., KIM K.S., GERTON G.L.;
OLSON G.E., KIM K.S., GERTON G.L.;
"AM67, a secretory component of the guinea pig sperm acrosomal matrix, is related to mouse sperm protein sp56 and the complement component 4-binding proteins.";
J. Biol. Chem. 273:12714-12722(1997).
EMBL; U75654; AAC13888.1; -.
HSSP; P10998; IVVC.
HSSP; P109084; sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U88576; AAB48622.1;
HSSP; P08603; 1HCC.
PFAM; PF00084; sushi; 4.
NON_TER 1 1
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STRAIN-HARTLEY; TISSUE-TESTIS;
MEDLINE; 97284752.
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SEQUENCE 347 AA; 37847 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 VNNDEGEWSGPPPEC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 234
                                                               136 NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHC--SDD--GFWSKEKPKCVEIS 191
218 CRQPHIPKG 226
                                                                                                                                                                                                                                                                 104 IIT-DLL-FGSTIEFSCSKGYSLIGSTT-SQCESQGKTVDWSDPLPECVIVKCDSPPDIS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 C-EVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVE 122
                                                                                                                              161 NGK-HSGT-DEDL-YTYGSLVTYVCDPNYSLLGNASISCLVANKTVGVWSSNPPTCEKVI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 18.6%; Score 293; DB 11; Length 533; Local Similarity 27.0%; Pred. No. 6.29e-49; hes 51; Conservative 51; Mismatches 69; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG- 115
                                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 18.8%;
Local Similarity 29.7%;
es 58; Conservative
                                                                                                                                                                                                     80 LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKCLPVTAPE 135
                                                                                                                                                                                                                                                                                                                                    21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS 175
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                                                                                                                                                                                                                                                                                                                                                                          ETNFRTGTALKYNCHRGYWRVNSSHVICDINGSWI-YNVF--CAKKRCRNPGELANGKVE 103
                                                                                                                                                                                                                                                                                                                                    DQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 28 F
29 533 A
533 AA; 59772 MW;
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ACROSOMAL MATRIX COMPONENT AM67.

; 60EEA526 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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QY 192 CKSPDVING 200

Search completed: Thu Jun 8 21:39:08 2000 Job time: 26 secs.

(TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:38:12 2000; MasPar time 8.92 Seconds 706.532 Million cell updates/sec

Tabular output not generated.

Title: >US-09-316-163-9
Description: (1-207) from US09316163.pep
Perfect Score: 1573

Sequence: 1 EDCNELPPRRNTEILTGSWS.....VEISCKSPDVINGSPISQKI 207

Scoring table: PAM 150 Gap 11

rched: 83857 segs, 30454973 residues

Post-processing: Minimum Match 09 Liscing first 45 summaries

Database: Swiss-prot38

Statistics: Mean 42.607; Variance 59.776; scale 0.713

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

			×
19 20 21 23	12 14 15 16 17	1 2 3 3 4 4 7 8 8 9 10 11	Result
280 279 276 272	290 288 288 286 287 284 284	1573 1154 308 308 303 303 303 303 297 298 298	Score
17.8 17.7 17.5 17.3	18.4 18.3 18.3 18.2 18.2 18.2	100.0 73.4 19.6 19.3 19.3 19.3 18.9 18.9 18.9	% Query Match
507 611 1019 958		1231 1234 484 830 263 768 768 345 345 345	Length
			DB
DAF_CAVPO LEM2_CANFA LFC_TACTR HIG_DROME APOH_HUMAN	CC4BP_HUMAN CCPH_HSVSA LEM2_MOUSE LEM2_RAT LEM2_RABIT DAF_PONPY MCP_HUMAN	CFAH_HUMAN CFAH_MOUSE LEM2_PIG LEM3_HUMAN VCP_VACCV LEM3_MOUSE LEM3_RAT APOH_MOUSE LEM4_HUMAN APOH_BOVIN DAF_HUMAN	ID
COMPLEMENT DECATACED E-SELECTIN PRECURSOR ( LIMULUS CLOTTING FACTO LOCOMOTICN-RELATED PRO BETA-2-GLYCOPROTEIN I	CAB-BINDING PROTEIN AL COMPLEMENT CONURDL PRO E-SELECTIN PRECURSOR ( E-SELECTIN PRECURSOR ( E-SELECTIN PRECURSOR ( COMPLEMENT DECAY-ACCEL MEMBRANE COFACTOR PROT	PR PR ( CELL ( C	Description
4.40e-46 2.72e-45 3.07e-44 1.03e-43	1.82e-48 1.82e-48 6.17e-48 3.35e-48 3.35e-47 1.30e-46		Pred. No.

45	44	43	42	41	40	39	38	37	36	ဌ	34	ω	32	31	30	29	28	27	26	25	24
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12.5	13.0	13.9	14.0	14.0	14.0	14.0	14.7	14.7	14.8		15.1	16.0	16.1	16.3	16.5	16.8	16.8	16.9	17.0	17.2	17.2
330	661	372	372	372	372	372	372	372	646	297	407	769	390	1025	558	469	345	485	2039	1033	610
Н	-	۰		щ	<u>_</u>	Н	Н	Н	$\vdash$	Н	$\vdash$	ш	Н	Н	ட	μ	μ	ب	-	μ.	$\vdash$
CFH1_HUMAN	F13B_HUMAN	LEMI FONET	LEMI_HUMAN		LEM1_MACMU	LEM1_PANTR	LEM1_MOUSE	LEM1_RAT	LEM3_BOVIN	APOH_RAT	DAF2_MOUSE	LEM3_SHEEP	DAF1_MOUSE	CR2_MOUSE	C4BP_RAT	C4BP_MOUSE	APOH_CANFA	LEM2_BOVIN	CR1_HUMAN	CR2_HUMAN	C4BP_BOVIN
COMPLEMENT FACTOR H-L1		L'OBLECTIN EXECUSEUS (								BETA-2-GLYCOPROTEIN I	COMPLEMENT DECAY - ACCEL	P-SELECTIN PRECURSOR (			G PROTEIN			E-SELECTIN PRECURSOR (	RECEPTOR ET	RECEPTOR TI	3 PROTEIN AL
4.1/e-25	1.040-21	7 0 40 - 27	3 510-30	7 000-31	7 000-31	7.896-31	1.290-31	7.15e-34	3.986-04	6.80e-33	2.096-35	9.000		1. UOC -40		7. TTE-42		1. LUC-4.	10.01.0	T. 000 - 40	1.03e-43

# ALIGNMENTS

RRRRRR	RY RT RX	R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	A COOOR	RESULT
SEQUENCE OF 19:35.  MEDLINE: 83048213.  Sim R.B., Disciplo R.G.;  Furification and structural studies on the complement-system control protein beta 1H (Factor H).";	SEQUENCE OF 1047-1231 FROM N.A.  MEDLINE; 91201892.  Estaller C., Kolstinen V., Schwaeble W., Dierich M.P., Weiss E.H.;  "Cloning of the 1.4-kb mRNA species of human complement factor H  "cloning of the index of the short consensus repeat family related to the carboxy terminal of the classical 150-kDa molecule.";  J. Immunol. 146:3190-3196(1991).	ELT. J. Immunol. 16:1351-1355(1986)  [3].  [3].  [3].  [4].  [5].  [5].  [5].  [5].  [5].  [5].  [5].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [6].  [7].  [8].  [8].  [8].  [9].  [1].  [1].  [1].  [1].  [1].  [2].  [2].  [3].  [4].  [1].  [1].  [1].  [2].  [2].  [3].  [4].  [4].  [1].  [2].  [3].  [4].  [4].  [6].  [7].  [8].  [8].  [8].  [8].  [8].  [9].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [2].  [1].  [2].  [3].  [4].  [4].  [4].  [6].  [7].  [8].  [8].  [8].  [9].  [9].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [1].  [2].  [1].  [1].  [1].  [2].  [1].  [2].  [1].  [2].  [1].  [2].  [2].  [3].  [4].  [1].  [2].  [1].  [2].  [2].  [2].  [3].  [4].  [4].  [4].  [7].  [8].  [8].  [8].  [8].  [9].	UENCE FRO SUE-LIVER LINE; 881 oche J. e complet e complet chem. J. UENCE OF ULIZ T.F. ulz T.F. unan compl	08, Created) 13, Last sequence updat 39, Last annotation upo H PRECURSOR. an). ar) Chordata; Craniata; 's; Catarrhini; Hominida	1

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EMBL; Y00716; CAA68704.1; -...
EMBL; X04697; CAB41739.1; ALT_FRAME.
EMBL; M65294; AAA35948.1; -...
PIR; S00254; NBHUH
PIR; S00254; NBCHUH
PIR; S00254; S00254.
PIR; S003013; S03013.
PDB; 1HCC; 15-APR-92.
PDB; 1HFH; 15-JUL-93.
PDB; 1HFH; 15-JUL-93.
PDB; 11471; 15-JUL-93.
PDB; 11471; 15-JUL-93.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        magnetic resonance.";
J. Mol. Biol. 232:268-284(1993).

-i. FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEXENT PATHWAY.

-i. SIMILARITY: CONVAINS 20 SUSHI (SCR) REPEATS.

-i. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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Barlow P.N., Steinkasserer A., Norman D.G., Kieffer B., Wiles A.P. Sim B., Campbell I.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Solution structure of a pair of complement modules by nuclear
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"Solution structure of the fifth repeat of factor H: a second example of the complement control protein module.";
Biochemistry 31:3626-3634(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barlow P.N., Norman D.G., Steinkasserer A., Horne T.J., Pearce J., Driscoll P.C., Sim B., Campbell I.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 264-322 (SUSHI 5).
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Norman D.G., Barlow P.N., Baron M., Day A.J., Sim B., Campbell I.D., "Three-dimensional structure of a complement control protein module in solution.";

J., Mol. Biol. 219:717-725(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 927-985 (SUSHI 16).
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                                                                                                                                                                                                                                                       3D-structure;
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                                                                                                                                                                                                                                                  alternate pathway; Plasm-structure; Polymorphism.
                                      SUSHI
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                      139125 MW; C65EC8CF8800B3FD CRC64;
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H -> Y
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C -> Q (IN REF. 3).
T -> V (IN REF. 3).
T -> Q (IN REF. 3).
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P06909;
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01-JAN-1988 (Rel. 06, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT FACTOR H PRECURSOR (PROTEIN BETA-1-H).
                                                                                                                                                                                                                                                       Munoz-Canoves P., Tack B.F., Vik D.P.; "Analysis of complement factor H mRNA expression: dexamethasone IFN-gamma increase the level of H in L cells."; Biochemistry 28:9891-9897(1989).
                                                                                                                                "Demonstration of an unusual allelic variation of mouse factor H by the complete cDNA sequence of the H.2 allotype.";

Immunol. 144:358-362(1990).

-i- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION COPENS AND THE ALTON OF COMBERGES. THE RATE OF DISSOCIATION OF COMBERGES. AND THE (COB) BB COMPLEX (CONVERTASE) AND THE (COB) BB COMPLEX (CONVERTASE) AND THE COB) BB COMPLEX (CONVERTASE) AND THE COMPLEMENT PATHWAY.

-i- POLYMORPHISM: TWO CODOMINANT ALLELES OF FACTOR H ARE PRESENT IN
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                               MEDLINE; 90148935.
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-19 FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                            "Murine protein H is comprised of 20 repeating units, in length.";
                                                                                                                                                                                                                                                                                                                                                                Kristensen T.,
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 86233353.
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EMBL; M12660; AAA37759.1; -. EMBL; J02891; AAA37795.1; -. EMBL; M31979; AAA37762.1; -.
                               or send an email to license@isb-sib.ch).
                                              use by non-profit modified and this st entities requires a
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                                                                                                                                                                                                            Moriwaki K.;
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                                                  Swiss Institute or Swiss Institute. There Bioinformatics Institutions as long as inprofit institutions as long as this statement is not removed. I
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                                                                                                                                                                                                                                                                                                                                      Tsang Y.T.M., Haskard D.O., Robinson M.K.; "Cloning and expression kinetics of porcine vascular cell adhesion molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-AORTIC ENDOMEDLINE; 94271236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-AORTIC ENDOTHELIUM;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
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P98110;
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"Molecular and functional analysis of porcine E-selectin reveals a potential role in xenograft rejection.";
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EDLINE; 95071392.
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                                                                                                                GLYCOLIPIDS).

FUNCTION: PLAYS AN IMPORTANT ROLE IN ACUTE CELLULAR ALLOGRAFT REJECTION. AND PROBABLY ALSO I NIXENGRAFT REJECTION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

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SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS; PORCINE E-LECTIN LACKS
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Pred. No. 6.87e-299;
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PFAM; PF00084; sushi; 4.
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PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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81 TGGNVFEYGVKAV--YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENG
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                                                 QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQNGDVSC 253
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                                                                                                         484 AA;
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Pred. No. 8.32e-54;
38; Mismatches 82
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313 -LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQCQWTQEVPSCQVVQCSSLEV 371

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  LEM3_HUMAN STANDAKU;

P16109;

P16109;

O1-APR-1990 (Rel. 14, Created)

O1-AUG-1990 (Rel. 15, Last sequence update)

15-JUL-1990 (Rel. 38, Last annotation update)

P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)

P-SELECTIN PRECURSOR (GRANULE ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnston G.I., Cook R.G., McEver R.P.; "Cloning of GMP-140, a granule membrane protein of platelets and endothelium: sequence similarity to proteins involved in cell adhesion and inflammation.";
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Finkarvota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                       Ruidavets J.B., Arveller D., Luc G., Cambien F.;

Ruidavets J.B., Arveller D., Luc G., Cambien F.;

"The P-selectin gene is highly polymorphic: reduced frequency of the pro715 allele carriers in patients with myocardial infarction.";

Hum. Mol. Genet. 7:1277-1284(198).

-i- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS FOR CARBONYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INVERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS STAYLYL-LEWIS X.

-i- SUBSCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL AND TO THE PALADE BODIES OF ENDOTHELIAL CELLS.
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Bajorath J., Stenkamp R., Aruffo A.;

"Knowledge-based model building of proteins: concepts and examples.";

Protein Sci. 2:1798-1810(1993).
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                                                                                                                                                                     This SWI
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                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; M60234; AAA35910.1; EMBL; M60217; AAA35910.1;
                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                            SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 9 SUSHI (SCR) REPEATS.
DATABASE: NAME-PROW; NOTE-CD guide CD62P entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
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M60222; AAA35910.1;
M60223; AAA35910.1;
M60224; AAA35910.1;
M60224; AAA35910.1;
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PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                   Motwal G.J., Moss B.;

Motwal G.J., Moss B.;

"Analysis of a large cluster of nonessential genes deleted

vaccinia virus terminal transposition mutant.";

Virology 167:524-537(1988).
                                            MEDLINE;
                                                            STRAIN-COPENHAGEN;
                                                                                                                                                                                                                                                                                                                         Kotwal G.J., Moss B.;
"Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.";
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  STRAIN-WR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN 35)
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccinia virus (strain WR), and Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCP_VACCV
P10998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROTEIN C3) (28 KD PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 APAPYCKAYQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 ECGELELPQHV-LMNCSHPLGNFSFNSQCSFHCTDGYQVNGPSKLECLASGIWTN-KP-P 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 55; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEENHCSDD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFWSKEKPKCVEISCKSPDV-INGS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHWSAPLPTCEAISCEPLESPVHGS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
             S.J., Johnson G.P.,
                                          91021027
                                                                                                                                                                                                                                                                                                                                                                                                                                           88318974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90844 MW;
     Perkus M.E., Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 308; DB 1;
Pred. No. 8.32e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T -> P (REDUCED FREQUENCY IN PATIENTS WITH MYOCARDIAL INFARCTION).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR_004195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId-VAR_004194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBC407BA2579F6EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
S.W., Winslow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 830;
                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
  J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Local
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                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                        DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                 Signal;
                                                                                                                                                                                                                                                                                                                                                      PDB; 1VVC; 03-DEC-97.
PDB; 1VVD; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M22812; AAA69605.1;
EMBL; M35027; AAA47997.1;
PIR; A31005; WMVZSP.
PDB; IVVC; 03-DEC-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X13166; CAA31564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENT ACTIVATION.";

J. MOI. Biol. 272:253-265(1997).

-I- FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

-I- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (BCA).

-I- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                         REPEAT
20 SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                          40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wiles A.P., Shaw G., Bright J., Perczel A., Campbell I.D. Barlow P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody-dependent complement-enhanced neutralization of infectivity and contributes to virulence."; Proc. Natl. Acad. Sci. U.S.A. 89:628-632(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "NMR studies of a viral protein that mimics the regulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 146-263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoletti E.;
"The complete DNA sequence of vaccinia virus.";
Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isaacs S.N., Kotwal G.J., Moss B.;
"Vaccinia virus complement-control protein prevents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goebel S.J., Johnson G.P., Perkus M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92115714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLETE GENOME
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                          Repeat; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97446168
                                                                                                                    263 AA;
                                                             Conservative
                                                                          19.3%;
                                                                                                                  28629 MW;
                                                                                                                                                                                                                                                                                                                                         3D-structure.
                                                             28;
                                                                        Score 303; DB 1;
Pred. No. 1.82e-52
                                                                                                                                           SUSHI 1.
SUSHI 2.
SUSHI 2.
SUSHI 3.
SUSHI 4.
BY SIMILARITY
                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                          COMPLEMENT CONTROL PROTEIN.
                                                                                                              E4322CC9A6EF8997 CRC64;
                                                                                                                                                                                                                                                                                             X SUSHI (SCR) REPEATS
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Davis S.W., Winslow J.P.,
                                                          76;
                                                                                  Length 263;
                                                       Indels 18;
                                                    Gaps
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weller A., Isenmann S., Vestweber D.; "Cloning of the mouse endothelial selectins. Expression of both E-and P-selectin is inducible by tumor necrosis factor alpha."; J. Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q01102;
                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanders W.E. Jr., Wilso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; vertebrata; mamm
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SELP OR GRMP.
MGD; MGI:98280; SELP.
PRINTS; PRO0343; SELECTIN.
PROSITE; PSO0022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
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                                                                                                                                                  HSSP;
                                                                                                                                                                                  EMBL; M72332; AAA37712.1; -. PIR; A42755; A42755.
                                                                                                                                                                                                                                          EMBL; M87861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STORED I MEMBRANE PROTEIN.
SISSUE SPECIFICITY: STORED INTER ALPHA-GRANULES OF PLATELETS
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
THE HUMAN SUSHI-2 EQUIVALENT.
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THE CELL SU
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                                                                                                                                                         P16109; 1FSB
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92340571.
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V.E. Jr., Wilson
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s of in vivo expression of murine P-
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PFAM; PF00008; lectin_c; 1.
PFAM; PF00084; sushi; 8.
Cell adhesion; Transmembrane;
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TEM3_RAT STANDARD; PRT; 768 AA.

p98106;
p01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
p-selectin precursor (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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                                                                                                               277 HPIAAFAYDSSCKFECQPGYRARGSNTLHCTGSGQWSEPLPTCEAIACEPPEIPIHGS 334
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                                                                                                                                   FEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAM 144
                                                                                                                                                                         Similarity 39; Conser
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Pred. No. 1.82e-52;
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A -> E (IN REF. 2).
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PROSITE; PS01186; EGF 2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PFAM; PF00059; lectin_c; 1.

PFAM; PF00084; sushi; 8.

Cell adhesion; Transmembrane; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, sequence comparison and in vivo expression encoding rat P-selectin.";
Gene 145:251-255(1994).
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Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Chordata; Craniata; Vertebrata; Mammalia;
Craniata; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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   AAA60325.1; -.
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01-APR-1993 (Rel. 25, C
01-APR-1993 (Rel. 25, L
15-JUL-1999 (Rel. 38, L
BETA-2-GLYCOPROTEIN I P
Kristensen T.;
"Structure of the human beta-2-glycoprotein I gene.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
                                                                                                                                                                                                       MEDLINE; 94242017.
Sellar G.C., Steel D w
                                                                                  SEQUENCE FROM N.A. STRAIN=BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                   APOH OK DACKTON (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verrepiaca.
Eukaryota; Metazoa; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                     glycoprotein
                                                                                                                                                                                                                                                                                                                                  "Molecular cloning of mouse beta 2-glycoprotein I and mapping of the gene to chromosome 11.";
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 92372000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN C-BINDING PROTEIN)
APOH OR B2GP1.
                                                                                                                                     "Characterization, expression and evolution of mouse bewalycoprotein I (apolipoprotein H)."; Blochem. Biophys. Res. Commun. 200:1521-1528(1994).
                                                                                                                                                                                                                                                                                                                          Genomics
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                                                                                                                                                                                                                     Steel D.M., Zafiropoulos A., Seery L.T.
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Last annotation update)
PRECURSOR (APOLIPOPROTEIN H)
TEIN) (APC INHIBITOR) (B2GPI).
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ENDOCYTOSIS SIGNAL
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No. 1.82e-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 AA
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CRC64;
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Best Local
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EMBL; S70439;
EMBL; Y11356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIGNAL 1
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    p16581; p16111;
01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM.)
                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                    LEM2_HUMAN
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                                                                                                                             154 KDYRPSAGNNSLYQDTVVFKCLPHFAMIGNDTVMCTEQGNWTRL-PECLEVKCPFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A43286; NBMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:88058; APOH.
                                                                                                                                                                                                          SYDPGEQIVYSCKPGYVSRGGMRRFTCPLTGMW-PINTLR-CVPRVCPFAGILENGIVRY
                                                                              ø
                                                                                                           VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP
                                                                                                                                                 TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                    TS---FEYPKNISFACNPGF-FLNGTSSSKCTEEGKWSPDIPACARITCPPPPYPKFALL 153
                                                                                                                                                                                       TYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00084; sushi; 4
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                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                     345
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F
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19
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BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                        Score 297; DB 1;
Pred. No. 7.31e-51;
                                                                                                                                                                                                                               37; Mismatches
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IHSUS
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                                                                      PRT;
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    (LECAM2)

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                                                                                                                                                                                                                                 Gaps
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A VE S.Q., Usher D., Virgil D., Zhang L.Q., Yochim S.E., Guptt P StI polymorphism detects the mutation of serine-128 to a pstI polymorphism detects the mutation of serine-128 to a confidence of the sering disease.";

J. Biomed. Sci 6:18-2(1999).

-I- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELL MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIVE ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVAL POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMIN GLYCOLIPIDS).

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATING THE HIGHER RISK OF CORONARY ARTERY DISEASE (CAD). A SIGNIFIC HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
Phillips
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins T., Williams A., Johnston G.I., Gimbrone M.A. Jr., Bevilacqua M.P.; "structure and chromosomal location of tleukocyte adhesion molecule 1."; J. Biol. Chem. 266:2466-2473(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bevilacqua M.P., Stengelin S., Gimbrone M.A. Jr., Seed B. "Endothelial leukocyte adhesion molecule 1: an inducible neutrophils related to complement regulatory proteins and Science 243:1160-1165(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Primates; Catarrhini; Hominidae;
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Hakomori S., Paulson J.C
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                                                                                                                                                                                                                                                                                                                                                                                                       Wenzel K., Felix S., Kleber F.X., Brachold R., Menke T., Schulte K.L., Glaser C., Rohde K., Baumann G., Speer A., "E-selectin polymorphism and atherosclerosis: an associat Hum. Mol. Genet. 3:1935-1937(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graves B.J., Crowther R.L., Chandran C., Rumberger J.M., Li. Huang K.-S., Presky D.H., Familletti P.C., Wolitzky B.A., Bur Transight into E-selectin/ligand interaction from the crystal structure and mutagenesis of the lec/EGF domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 89162047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Endothelial leukocyte adhesion molecule 1: direc
and functional interactions.";
aroc. Natl. Acad. Sci. U.S.A. 87:1673-1677(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ligand,
                                                                                                                                                                                                                                                                                                                                VARIANT ARG-149.
MEDLINE; 99134508.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "ELAM-1 mediates cell adhesion by 
ligand, sialv1-Lex.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nudelman E., Gaeta F.C., Perez
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                                                                                                                                                                                                                ENDOTHELIAL CELLS
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                                                              IS ASSOCIATED WITH A
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                    PATIENTS
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PFAM; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED WITH UNSELECTED POPULATION (SER-149).

SIMILACTE? FOOTHER SELECTINS/LECAMS.

SIMILARITY: FOOTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.

SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.

DATABASE: NAME-PROW; NOTE-CD guide CD62E entry;
WWWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62e.htm".
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M61893, AAA52375.1;
M61895, AAA52375.1;
M61888, AAA52375.1;
M61888, AAA52375.1;
M61890, AAA52375.1;
M61891, AAA52375.1;
M61892, AAA52375.1;
M61892, AAA52375.1;
M61892, AAA52375.1;
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A35046; A35046.
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Transmembrane;
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                 Repeat;
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SUSHI 1.
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SUSHI 5.
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C-TYPE LECTIN (SHORT FORM)
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POTENTIAL.
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at; Polymorphism;
           Y SIMILARITY.
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Best Local
                                                                   Kato H., Enjyoji K.-I.; "Amino acid sequence and location of the disulfide bonds in beta 2 glycoprotein I: the presence of five Sushi domains.", Biochemistry 30:11687-11694(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APOH_BOVIN STANDARD; PRT; 345 AA. P17690; Q28052; Q1-AUG-1990 (Rel. 15, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN
                     SEQUENCE OF 20-41.
MEDLINE; 90226328.
                                                                                                                                                                                                                     "Complete primary structure of bovine beta localization of the disulfide bridges."; Biochemistry 31:3611-3617(1992).
                                                                                                                                                                                                                                                                                         MEDLINE; 92232647.
Bendixen E., Halkier T., Magnusson S.,
                                                                                                                                                                                                                                                                                                                                                                                                          Gao B., Virmani M.,
Appella E., Kunos G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
SEQUENCE
                                                                                                                                                     MEDLINE;
                                                                                                                                                                          TISSUE-PLASMA;
                                                                                                                                                                                    SEQUENCE OF 20-345,
                                                                                                                                                                                                                                                                                   Kristensen T.;
                                                                                                                                                                                                                                                                                                                                        TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4-345 FROM N.A., PARTIAL SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; mammaila;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGEVECEQUPGSFFWNTT 267
                                                                                                                                                                                                                                                                                                                                                                                        ppella E., Kunos G., Takacs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFT-LTGGNVFEYGVK
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Esch F., Congote L.F.;
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Pred. No. 3.95e-51.
33; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                         Lazar-Wesley E., Sakaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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H -> Y (IN REF. 2).
7D43E3COD1229229
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                                                                                                                                                                                    SITES,
                                                                                                                                                                                                                                                      2-glycoprotein
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                                                                                                                                                                                  DISULFIDE BONDS
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                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
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153 LSVYKPLAGNNSFYGSKAV-FKCLPHHAMFGNDTVTCTEHGNWT-QLPECREVRCPFP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEBARIN, PHOSPHOLLPIDS, AND DEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.

TISSUE SPECIFICITY: PLASMA.
SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                 39
                     08
                                        97
                                                             22
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                                                                                RTYEPGEQIVFSCQPGYVSRGGIRRFTCPLTGLW-PINTL-KCMPRVCPFAGILENGTVR 96
                    LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGK 138
                                        YT---TFEYPNTISFSCHTGFYLKGASSAK-CTEEGKWSPDLPVCAPITCPPPPIPKFAS 152
                                                            QTYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00084; sushi; 4.
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                                                                                                                Similarity
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lch inhibits thymidine incorporation in fetal calf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
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29.8%;
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                                                                                                       36;
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SUSHI 1.
SUSHI 2.
                                                                                                                                                       BETA-2-GLYCOPROTEIN I
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(IN REF. 1).
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(IN REF. 1).
C (IN REF. 1).
N (IN REF. 1).
N (IN REF. 1).
PR (IN REF. 1).
TO REF. 1.
                                                                                                      Mismatches
                                                                                                                292; DB 1;
No. 1.57e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                 432F
                                                                                                                           Length 345;
                                                                                                       Indels
                                                                                                      12;
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RESULT TO SEE THE SEE 
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Medof M.E., Lublin D.M., Holers V.M., Ayers D.J., General M.L.;

Leykam J.F., Atkinson J.P., Tykocinski M.L.;

Leykam d.F., Atkinson J.P., Tykocinski M.L.;

"Cloning and characterization of cDNAs encoding the complete sequence of decay-accelerating factor of human complement.";

of decay-accelerating factor of human complement.";

n=n Matl. Acad. Sci. U.S.A. 84:2007-2011(1987).
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Creat
01-FEB-1996 (Rel. 33, Last
01-NOV-1997 (Rel. 35, Last
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Nature 325:545-549(1987).
[2]
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                                                                                                                                                                                                                                                                                                                   MEDLINE;
Ward T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nussenzweig V.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete determination of disulfide bonds in consensus repeat units of decay accelerating Biochim. Biophys. Acta 1116:235-240(1992).
                                                                                                                                                                    "Decay-accelerating factor CD55 is identified as the receptor for echovirus 7 using CELICS, a rapid immuno-focal cloning method."; EMBO J. 13:5070-5074(1994).
                                                                                                                                                                                                                                                                           Ward T., Pipkin P.A., Clarkson N.A., Almond J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakano Y., Sumida K., Kikuta N., Miura N.-H., Tobe T., Tomita M.; "Complete determination of disulfide bonds localized within the short consensus repeat units of decay accelerating factor (CD55 antigen).";
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                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION AS A ECHOVIRUS RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
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Lublin D.M., Mallinson G., Ferdman B.R., Telen M.J., l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFIDE BONDS
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                                                                     MEDLINE;
                                                                                                      VARIANT BLOOD GROUP DR(A-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ycophospholipid membrane anchor attachment.
cleavage/attachment site.";
Biol. Chem. 266:1250-1257(1991).
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ion of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             decay-accelerating factor gene
Anstee D.J.
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       Reid M.E., Thompson , Tanner M.J.A.;
                                                                                                                                                                                                                                                                                                                       Stone D.M., Minor P.D.,
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of.

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EMBL; M31516; AAA52169.1; -.
EMBL; M30142; AAA52168.1; -.
EMBL; M15799; AAA52167.1; -.
EMBL; M64653; AAA52170.1; -.
EMBL; M64356; AAA52170.1; JOIN
EMBL; S72858; AAC60633.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPES THAT ARE IN INTIMATE CONTACT WITH PLANMA COMPLEMENT
PROTEINS. IT IS ALSO FOUND ON THE SURFACES OF EPITHELIAL CELLS
LINING EXTRACELLULAR COMPARTMENTS, AND VARIANTS OF THE MOLECULE
ARE PRESENT IN BODY FLUIDS AND IN EXTRACELLULAR MATRIX.

-!- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
ACTIVE SITE ON SCR3 (BY SIMILIARITY).

-!- PTM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.
-!- POLYMORPHISM: DAF IS RESPONSIBLE FOR THE CROMER BLOOD GROUP
SYSTEM. IT CONSISTS OF AT LEAST SEVEN HIGH-INCIDENCE (CR(A),
TC(A), DR(A), ES(A), WES(B), UMC, AND IFC) AND LOW-INCIDENCE
(TC(B), TC(C), AND WES(A)) ANTIENS THAT RESIDE ON DAF. IN THE
CROMER PHENOTYPES DR(A-) AND INAB THERE IS REDUCED OR ABSENT
PHENOTYPE, A SINGLE NUCLEOTIDE SUBSTITUTION WITHIN EXON 5 ACCOUNTS
FOR TWO CHARGES: A SIMPLE AMINO ACID SUBSTITUTION THAT IS THE
BASIS OF THE ANTIGENIC VARIATION, AND AN ALTERNATIVE SPLICING
EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
DHENOTYPE
                                                                                                   PFAM; PF00084; sushi; 4.
Complement pathway; Plasma; Glycoprotein;
Alternative splicing; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular basis of reduced or absent expression of decay accelerating factor in Cromer blood group phenotypes."; Blood 84:1276-1282(1994).

-i- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION. INTERPRACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES INTERPERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS THE FORMATION OF C4B2A AND C3BBB, THE AMPLIFICATION CONVERTASES OF THE CONFLEMENT CASCADE.

-i- FUNCTION: ALSO ACTS AS THE RECEPTOR FOR ECHOVIRUS 7 AND RELATED VIRUSES (ECHOVIRUSES 13, 21, 29 AND 33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIRUSES (ECHOVINUSES 13, 21, 29 AND 33).

-i- SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT HOMODIMER (MINOR FORM).

-i- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.

-i- ALTERNATIVE PRODUCTS: TWO FORMS OF DAF (DAF-2, SHOWN HERE, AND DAF-1) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

-i- TISSUE SPECIFICITY: EXPRESSED ON THE PLASMA MEMBRANES OF ALL CELL
                                                                                                                                                                                                ; A39101; A39101;

3; S23138; S23138;

3P; P08603; 1HCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATABASE: NAME-PROW; NOTE-CD guide CD55 entry; www-"http://www.ncbi.nlm.nih.gov/prow/cd/cd55.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS SIMILARITY: BELONGS TO THE RECEPTORS OF CON
                                                                                                                                                                                                                                                                          S16187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RCA) FAMILY
                                                                                          group antigen.
                                                                                                                                                                                                                                                S16187.
A39101:
                                                                                                                                                                                                                                                                                                                                      ; -.
; JOINED.
; -.
COMPLEMENT DECAY-ACCELERATING FACTOR. REMOVED IN MATURE FORM.
4 X SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF.
                                                                                                     Membrane; Repeat;
Sushi; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENT ACTIVATION
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RESULT

AC PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.; "Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein."; Biochem. Biophys. Res. Commun. 165:138-144(1989).
                                                                                                                                                                                                                                                                                                              P04003;
23-OCT-1986 (Rel. 02, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
SEQUENCE
                                                                                                     MEDLINE; 90073699.
                                                                                                                          TISSUE=LIVER;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                            C4BPA OR C4BP.
                                                                                                                                                                                                                                                                                                     C4B-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                  C4BP_HUMAN
                                                                                                                                                                                             Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 VNNDEGEWSGPPPEC 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 C-EVPTRINSASIKQPYITQNYFPYGTVVEYECRPGYRREPSISPKLTCLQNIKWSTAVE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CNELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 268
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58; Conse
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85
381 AA;
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PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                    Chordata; Craniata;
Catarrhini; Hominida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 293; DB 1;
Pred. No. 8.51e-50;
43; Mismatches 75
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R -> L (IN TC(B) ANTIGEN).

/FIId=VAR_001997.

R -> P (IN TC(C) ANTIGEN).

/FIId=VAR_001998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T -> I (IN REF. 1).
S -> M (IN REF. 2).
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HTCFTLTGLLGTLVTMGLLT -> SRPVTQAGMRWCDRSSLQSRTPGFKRSFHFSLPSSWYYRAHVFHYDRFAWDASNHGLA
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SUSHI 2.
SUSHI 3.
SUSHI 4.
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/FTId-VAR_002000
A -> P (IN CR(A-) ANTIGEN)
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/FTId=VAR_001999.
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                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                597
                                                                                                                                                                                                         Vertebrata; Mammalia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 19;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dahlback B., Smith C.A., Mueller-Eberhard H.J.;
"Visualization of human C4b-binding protein and its complexes with vitamin K-dependent protein and complement protein C4b.";
Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).

-i- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INCTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chung L.P., Gagnon J., Reid K.B.M.; "Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and malignment of the fragments produced by limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and characterization of the cDNA coding for C4b-molecular cloning and characterization of the classical pathway of the binding protein, a regulatory protein of the classical pathway of the human complement system."; Biochem. J. 230:133-141(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 203-288 FROM N.A. MEDLINE; 86301119. Lintin S.J., Reid K.B.M.; "Studies on the structure of the FEBS Lett. 204:77-81(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4b-binding protein and interspecies cDNA sequence.";
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Lintin S.J., Lewin A.R., Reid A.B.M.,
"Derivation of the sequence of the signal peptide in human
"Derivation of the sequence of the signal peptide in human
"Derivation of the sequence of the signal peptide in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolysis with chymotrypsin and the peptides produced by cyanogen bromide treatment.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun
                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 49-88
EMBL; M31452; AAA36507.1; -. EMBL; M62486; AAA36506.1; -.
                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE, MEDLINE; 83221615.
                                                                                                                                                                                                                                                                                               (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BCA COMPLEX (C3 CONVERTANCE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S AND WITH SEROM AMYLOID P COMPONENT.
SUBUNIT: DISSULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS OF 3 POSSIBLE SORTS: A 570 KD COMPLEX OF 7 ALPHA CHAINS AND 1 BET CHAIN, A 530 KD HOMOHEPTAMER OF ALPHA CHAINS OR A 500 KD COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF THE ALPHA CHAIN HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE BINDING SITE FOR C4B AT THE END.
                                                                                                                                                                                                                    SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.
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HSSP; P10998; 1VVC.
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182 RNGR--HSG-E-ENEYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKI
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M62481;
M62481;
M62481;
M62484;
M62485;
M62485;
X07853;
X04284;
X042865;
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M62476;
M62477;
M62478;
                                                                      FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYR-EC-DTD-GWTNDIPICEVVKCLPVTAP
                                                                                                                                                                                                      TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTFCIY-KR-CRHPGELRNGQ 123
                                                                                                                 VEIKT-DL-SFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPDI
                                                                                                                                                             SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT
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                                                                                                                                                                                                                                                                              Score 290; DB 1;
Pred. No. 5.35e-49;
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Y -> H.
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EMBL; X64346; CAA45627.1; --
EMBL; X60283; CAA42823.1; --
EMBL; X60283; CAA42822.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND A SECRETED ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
-!- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).
-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00084; sushi; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albrecht J.-C., Fleckenstein "New member of the multigene herpesvirus saimiri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newman C., Wittmann Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Albrecht J.-C., Nicholas J., Biller D., Camero
Newman C., Wittmann S., Craxton M.A., Coleman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY TO CCP.
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Viruses; dsDNA viruses, no RNA stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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oleman H., Fleckenstein B.,
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Q00690;
Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-FEB-1996 (Rel. 33, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
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                                                                                                                                                                                                                                                                                  Weller A., Isenmann S., Vestweber D.;

"Cloning of the mouse endothelial selectins. Expression of both E and P-selectin is inducible by tumor necrosis factor alpha.";

J. Biol. Chem. 267:15176-15183(1992).

-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES POLYLACTOSSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Delamarter J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Murine endothelial leukocyte-adhesion molecule 1 is a close structural and functional homologue of the human protein."; Eur. J. Biochem. 206:401-411(1992).
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                                                                                                                          GLYCOLIPIDS).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
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MISSING (IN SHORT ISOFORM).
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Best Local
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PROSITE; PS00122; EGE_1; 1.
PROSITE; PS01186; EGE_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                            DISULFID DISULFID DISULFID
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                                                                  242 ECEALT-HPAHGIRKCSSNPGSYPWNTTCTFDCVEGYRRVGAQNLQCTSSGIWDNETP-- 298
358 PQIPVCKAVQCEALSAPQQGNMKCLPSASGP-FQNGSSCEFSCEEGFELKGSRRLQCGPR 416
                                  299
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                                SCKAVTCDAIPOPONGFVSCSHSTAGELAFKSSCNFTCEOSFTLQGPAQV-ECSAQGOWT 357
                                                   DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P16581;
                  KCQKRPCGH-P-GDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
                                                                                     49;
                                                                                               Similarity
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                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lectin_c; 1. sushi; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SELE
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                                                                                              18.3%;
25.1%;
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                                                                                                                        MW;
                                                                                      42;
                                                                                                      Score 288;
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C-TYPE LECTIN (SHORT FO
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                                                                                                                                                                                                                                                                                                                                                                             IHSUS
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                                                                                                                                POTENTIAL
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                                                                                       Mismatches
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                                                                                               3; DB 1; 1
. 1.82e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                               (SHORT FORM)
                                                                                       95;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROSENDIOOM C.L., Auchampach J.A., Anderson D.C., Manning A.M.; Submitted (NOV-1993) to the EMBL/GenBank/DBDJ databases.

-I-FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKCCYTES. THE LIGAND RECOGNIZED BY ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SELE OR ELAM-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00084; sushi; 5. Cell adhesion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00022; EGF_1; 1.

PROSITE; PS00615; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1;

PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CD62E)
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                                                                                                          REPEAT
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SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L25527; AAA41113.1; -. P16581; 1KJA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sushi;
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Best Local Similarity 25.1%;
Matches 50; Conservative
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549 AA;
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60079 MW;
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Pred. No. 6.17e-48;
45; Mismatches 97; Indels
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jun 8 21:37:08 2000; MasPar time 8.38 Seconds 585.300 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-316-163-9 (1-207) from US09316163.pep 1573

Sequence: 1 EDCNELPPRRNTEILTGSWS.....VEISCKSPDVINGSPISQKI 207

Scoring table:

PAM 150 Gap 11

188963 segs, 23686106 residues

Post-processing: Minimum March 08 Listing first 45/summaries Database: a-gereseq36 geneseqp

Statistics:

Melan 31.247; Variance 114.255; scale 0.273

pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1 973 61.9 3 308 19.6 4 308 19.6 4 308 19.6 5 298 18.9 6 298 18.9 9 298 18.9 9 298 18.9 10 293 18.6 11 293 18.6 12 293 18.6 13 293 18.6 16 293 18.6 17 293 18.6 293 18.6	
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	Query Match
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W39154 W39155 W99899 W998916 R05116 R05494 R05538 R05538 W18839 W16733 W706881 W66881 W66881 W73505 W46733 P74048 P94774 W73505	ID
Human partial Compleme Clone pRRB9PH410 CFH r Porcine E-selectin. P-selectin. Endothelial cell-leuco Endothelial leukocyte Endothelial leukocyte Endothelial leukocyte Endothelial-leukocyte Eselectin. Amino acid sequence of Decay accelerating fac Human decay accelerating fac Human decay accelerating fac Decay accelerating fac Membrane bound decay accelerating fac Membrane bound decay accelerating Decay accelerating fac Membrane bound decay accelerating fac Membrane co-factor pro Human decay accelerating fac Membrane co-factor pro Membrane co-factor selections of the selection of the selec	Description
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CD46 from clone pm5.3. CD46 from clone pm5.10	n membrane construct	Membrane cofactor prot	Membrane cofactor prot Membrane co-factor pro		CD46 from clone pm5.1.	from clone pm5.	rane cofac	Human CD46.	CD46 construct subSCR3	Human MCP.	CD46 wild-type.	Porcine complement inn	Deduced sequence of co	Herpesvirus saimiri mc	membrane
. 95e-	4.25e-18	.32e-1	3.32e-18	.58e-	2.03e-18	2.03e-18	9.66e-19			9.66e-19	9.000-19	4.00E-19	2. BIE-19	1./10-13	

# ALIGNMENTS

Db 121 INGSPISQKI 130	旦
Qy 138 KIVSSAMEPDREYHFGQAVRFVCNSGYKLEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197	Ø
Db 61 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 120	מַ
Qy 78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENG 137	g
Db 1 FTLIGGNVFEYGVKAVYTCNEGYQLLGEINYRBCDTDGWTNDIPICEVVKCLPVTAPENG 60	멅
Query Match 61.9%; Score 973; DB 1; Length 240;	
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such proteins and a CFH antigens can be used in screening or ro	င္ပ
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in the identification of complement factor H	38
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Example 6B; Fig 6B; 104pp; Enc	PS
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by modulating or detecting tumour associated	PT.
Treating or screening for cancer, e.g. renal or urogenital car	PT:
N-PSDB; V02790.	ב ק
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PA (BAKU-) BAKU DIAGNUSIIC SCI INC. Trefiold DI Hass GM. Kinders RJ:	5 A
06-MAR-1997; US-038614.	PR
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16-OCT-1997.	PD
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09-APR-1997; US-812481.

09-APR-1996; US-015083.

09-APR-1996; US-030614.

06-MAR-1997; US-038614.

(BARD-) BARD DIAGNOSTIC SCI INC.

Enfield DL, Hass GM, Kinders RJ;

WPI; 97-512742/47.
                                    The present sequence is porcine E-selectin (E-sel). The nucleotide sequence encoding E-sel may be used in the diagnosis, prevention and treatment of tissue rejection following xenotransplants of pig organs and also in the monitoring (by specific measurement of the amount of
                                                                                                                                                         Nucleic acids encoding the porcine E-selectin protein - useful diagnosing and treating rejection of xenotransplanted pig organs Claim 1; Column 47-50; 30pp; English.
                                                                                                                                                                                                                                                                                               (ALEX-) ALEXION PHARM INC.
Evans MJ, Matis LA, Rollins S, Rother RP;
WPI; 99-253853/21.
                                                                                                                                                                                                                                                                              N-PSDB; X19809.
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01-JUN-1994; US-252493.
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Example 6B; Fig 6B; 104pp; English.

This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour-associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer agents that may modulate this antigen could be used in the manufacture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 AVREVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKI 207
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Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urogenital cancer; medicament; modulator
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Local Similarity 99.1%;
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in the blood of the patient) and modulation of immune
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Pred. No. 8.32e-82;
""smatches 0;
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γ 밁 20 밁

61 KCOKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYOLLGEINYRECDTDG-WT 117

QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313 DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60 Matches

Conservative

44;

Mismatches

94;

Indels 12;

Gaps

Local

199 ECGELELPOHV-LMNCSHPLGNFSFNSQCSFHCTDGYQVNGPSKLECLASGIWTN-KP-P 255

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Qγ
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02-MAR-1995.
19-AUG-1994; U09395.
20-AUG-1993; US-110158.
(OKLA) UNIV OKLAHOMA STATE.
MCEVEX RP, PAn J;
                                                                                                                        P-selectin gene - for regulating gene expression in engotherial cells and mega:karyocyte(s) bisclosure; Fig 1; 88pp; English.

The sequence is that of the P-selectin gene product from endothelial cells, determined from a composite of four overlapping cDNAs: lambda GMPE1-lambda GMPE4. The P-selectin gene or its fragments may be used GMPE1-lambda GMPE4. The P-selectin gene or its fragments may be used
                                                          to inhibit P-selectin expression, thus controlling inflammatory and haemostatic processes in e.g. rheumatoid arthritis, ischaemic injury bacterial sepsis, tumour metastases, atherosclerosis, etc. Sequence 830 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endothelium, contributes to the binding and subsequent transmigration of inflammatory cells into the graft tissue that occurs during acute cellular allograft rejection. Therefore, preventing expression of E-sel on the donor tissue may reduce the risk of rejection by modulating E-sel mediated cell adhesion. Fragments of the nucleotide sequence encoding E-sel may be used as polymerase chain reaction (PCR) primers or hybridization probes for the identification and/or isolation of the porcine E-sel gene from genomic DNA. Antisense sequences may be used to inhibit the expression of E-sel. DNA constructs may be used to introduce antisense sequences to a cell, or to inactivate the E-sel gene (e.g. knock-out constructs). Cells in which the expression of E-sel has been prevented may be used as disease models or to produce transplantation with
                                                                                                                                                                                                                                                 Expression control elements in the 5'- flanking region of the P-selectin gene - for regulating gene expression in endothel
                                                                                                                                                                                                                                                                                                      Mcever RP, Pan J;
WPI; 95-106847/14.
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04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Control elements; gene expression; endothelial cells; megakaryocytes; rheumatoid arthritis; ischaemic injury;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 -LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSSLEV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the transplants. Cytokine-induced expression of E-sel by donor organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQNGDVSC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 NHSSIGEFAYKSTCHFTCAEGFGLQGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQPKNG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 TGGNVFEYGVKAV--YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal Similarity
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    h 19.6%;
Similarity 26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial sepsis; tumour metastases
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Score 308; DB 1;
Pred. No. 1.19e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 308; DB 1;
Pred. No. 1.19e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                    Length 830;
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Combine protein possesses a hydrophobic N-terminal sequence contaracteristic of a signal sequence. It is predicted that the mature contaracteristic of a signal sequence. It is predicted that the mature contaracteristic of a signal sequence. It is predicted that the including contare in the polypeptide is ca. 554 amino acids including contains of the polypeptide is ca. 554 amino acids including contended by a hydrophobic transmembrane contains of 24 amino acids. It is noted that the protein contains claven N-glycosylation sites.

Contains be used to identify molecules which inhibit binding of claucocytes to cells, and such binding can be inhibited contains eleven n-glycosylation sites.

Contains and such binding can be inhibited contains eleven n-glycosylation sites.

Contains and such binding can be inhibited contains eleven n-glycosylation sites.

Contains and such binding can be inhibited contains eleven n-glycosylation sites.

Contains and such binding can be inhibited contains eleven n-glycosylation sites.

Contains and such binding can be inhibited contains eleven n-glycosylation sites.

Contains and such binding can be inhibited can be inhibited such contains eleven n-glycosylations and such binding can be inhibited can be under the protein contains eleven n-glycosylations and such binding can be inhibited can be inhibited such contains eleven n-glycosylations and such binding can be inhibited can be under the protein contains eleven n-glycosylations and such binding can be inhibited can be under the protein possesses a short, charged near the protein contains eleven n-glycosylations and such binding can be inhibited near the protein can be treated under the protein can be under the protein 
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27-APR-1990; U02357.
28-APR-1998; US-345151.
01-JUN-1989; US-35916.
18-DEC-1989; US-452675.
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pSQ148 and pSQ149.
Endothelial cell-leucocyte adhesion molecule 1; ELAM1; antibodies;
molecule involved in leucocyte adhesion; MILA; inflammation.
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Endothelial cell adhesion mols.
inhibition-detection of binding
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22-OCT-1990 (first entry)
Endothelial leukocyte adhesion molecule-1 (ELAM-1).
Endothelial leukocyte adhesion molecule; ELAM-1; inflamation;
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                                                                                                                                                    R05494 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268
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                                                                                                                                                                                                                                                                                                                                                                                          TFKSSCNFTCEEGFMLQGPAQVECTTQGQWTQQIPVCEAFQCTA 369
                                                                                                                                                                                                                                                                                                                    HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
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WO9005786-A.
31-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     injury, vasculitis etc. It may also be useful in treatment and diagnosis of leukaemia, lymphomas and metastic spread of tumour cells, as well as in mediation of cell-cell interactions in embryogenesis and organ development, in neoplasia, and wound and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in treating inflamation, post reperfusion injury, bacterial infection, vasculitis, leukaemia etc. Claim 13; 36; 54pp; English. ELAM-1 is useful in treatment of inflamation, post reper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q04910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bevilacqua MP, Grimbrone MA,
WPI; 90-193436/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1989; 005073.
14-NOV-1988; US-270873
                                                                                                                                                                                                                                                                                                                                                                                                    Endothelial-leukocyte adhesion molecule (ELAM-1).
Endothelial-leukocyte adhesion molecules; ELAM-1; cytotoxin;
cytokine; cancer; leukemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO-) Gen Hospital Corp
(BRIG-) Brigham Womens Hosp.
                                                            adhesion protein.

Disclosure; 44pp; English.

ELAM specific antibodies, attached to a suitable drug eg. a cytotoxin can direct the action of the drug to sites of inflammation, tissue damage and infection. The same Abs can be used to treat leukaemia, lymphoma, vasculitis and metastic spread of cancer cells. Labelled ELAM specific Abs can be used to detect expression of the adhesion molecules.

Sequence 610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R05538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia; lymphoma; metastasis; cancer;
                                                                                                                                                                                                                                                                      14-NOV-1989; 005075.
14-NOV-1988; US-270860.
(BRIG-) Brigham & Womens Ho.
Bevilacqua MP, Grimbrone MA;
WPI; 90-193270/25.
                                                                                                                                                                                                                                                                                                                                                                    WO9005539-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R05538 standard; protein;
                                                                                                                                                                                                        and for detecting expression of this endothelial leucocyte
                                                                                                                                                                                                                                       Antibodies against ELAM-1 to treat inflamation, infection,
                                                                                                                                                                                                                                                        N-PSDB; Q04776
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGFVECFQNPGSFPWNTT 267
                                                                                                                                                                                                                                                                                                                                                      31-MAY-1990.
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                                                                                                                                                                                                                          leukaemia
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y Match 18.9%; Local Similarity 27.4%; hes 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRPGYRSLGNVIMVCRK-GEWVALNPLRKCOKRPCGHPGDTPFGTFT-LTGGNVFEYGVK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFKSSCNFTCEEGFMLQGPAQVECTTQGQWTQQIPVCEAFQCTA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes expressing endothelial-leukocyte adhesion molecule-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 18.9%;
Similarity 27.4%;
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610
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Pred. No. 1.43e-20
Score 298; DB 1; L
Pred. No. 1.43e-20;
33; Mismatches 79;
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                               Length 610
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      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
W46733 standard; Protein; 610 AA W46733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is E-selectin (formerly known as endothelial leukocyte adhesion molecule-1; ELAM-1). E-selectin is identified by specific binding of murine monoclonal antibodies H4/18 and H8/7, developed against stimulated endothelial cells. New immunoconjugates of the invention comprise monoclonal antibody H18/7, or a fragment which binds to E-selectin conjugated to a therapeutic agent. The immunoconjugate is used to selectively target the therapeutic agent to activated endothelium expressing E-selectin, especially for treating inflammation, microbial infections, post-reperfusion injury, malignant tumours, vasculities vascular emotathemuscoperfusion injury, malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or acute or chronic allograft rejection. Sequence 610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-selectin; endothelial leukocyte adhesion molecule-1; ELAM-1; murine monoclonal antibody; H4/18; H18/7; immunoconjugate; activated endothelium; treat; inflammation; microbial infection; post-reperfusion injury; malignant tumour; vasculitis; vascular smooth-muscle cell proliferative disorder; acute;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumours, vasculitis, vascular smooth-muscle cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immuno:conjugates based on monoclonal antibody specific E-selectin - for targetting therapeutic agent to activate
                                                                                                                                                                               151
                                                                                                                                                                                                                                326 TFKSSCNFTCEEGFMLQGPAQVECTTQGQWTQQIPVCEAFQCTA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-DEC-1994; US-365470.
14-NOV-1988; US-270860.
13-MAR-1992; US-850802.
05-AUG-1993; US-102510.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Column 35-38; 36pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gimbrone MA;
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                                                                                                                                                                                                                                                                                                                                                                      268 CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGFVECFQNPGSFPWNTT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                             34 CRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFT-LIGGNVFEYGVK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326
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                                                                                                                                                                HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.98;
27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 298; DB 1;
Pred. No. 1.43e-20;
33; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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Best Local
                                                                                                                                                                               Homo sapiens. W09634965-A2. 07-NOV-1996.
peptide sequences
Disclosure; Page 25; 33pp; English.
                                                     Chimeric proteins for inhibiting complement-mediated cell lysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents human endothelial leukocyte adhesion molecule-1 (ELAM-1). ELAM-1 is a membrane glycoprotein which is induced by a number of cytokines. Pathological conditions associated with the overexpression of cellular adhesion molecules, such as ELAM-1 or intracellular adhesion molecule-1 (ICAM-1), can be treated with the novel pharmaceutical composition of the invention. The composition comprises an effective amount of an ICAM-1 antisense molecule encapsulated in a lipid mixture, the lipid mixture comprising at cationic lipids. The composition is used in a method to treat pathological conditions associated with overexpression of ICAM-1, such as Alzheimer's disease, multiple sclerosis, viral hepatitis,
                                         comprise membrane co-factor protein
                                                                                                   (CHIR ) CHIRON CORP
Creasey AA, Innis )
                                                                                                                                       03-MAY-1996; U06301.
05-MAY-1995; US-435149
                                                                                                                                                                                                                                           decay accelerating factor; DAF; chimeric protien; glycosaminoglycheparin; cell lysis; sepsis; adult respiratory distress; syndrome;
                                                                                                                                                                                                                                                                 Complement inhibitor; membrane co-factor protein; MCP; decay accelerating factor; DAF; chimeric protien; glycosaminoglycan;
                                                                                                                                                                                                                                                                                                                     W06881;
18-MAR-1997 (first entry)
                                                                                                                                                                                                                                   reperfusion injury; cell damage.
                                                                                                                                                                                                                                                                                                           Decay accelerating factor
                                                                                                                                                                                                                                                                                                                                                                  W06881 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for treatment of conditions associated with overexpression of ICAM-1 - used to treat e.g. Alzheime. glomerulonephritis, rheumatoid arthritis etc. Disclosure; Pages 44-46; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1998 (first entry)
Amino acid sequence of endothelial leukocyte adhesion molecule-1.
Endothelial leukocyte adhesion molecule-1; ELAM-1; inducible; cytokine; overexpression; cellular adhesion molecule; intracellular adhesion molecule-1; ICAM-1; antisense molecule; lipid mixture; Alzheimer's disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAX-1996; US-657753.
(UVBR-) UNIV BRITISH COLUMBIA.
HOPE MJ, Klimuk SK, Scherrer P, Semple SC;
WPI: 98-042180/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholangitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V16208
                                                                                                                                                                                                                                                                                                                                                                                                                                            151 HFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 CTFDCEEGFELMGAQSL-QCTSSGNWDNEKPTCKAVTCRAVRQPQNGS-VRCSHSPAGEF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 CDRGYLPSSMETMQCMSSGEWSA--PIPACNVVECDAVTNPANGFVECFQNPGSFPWNTT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 AVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 CRPGYRSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFT-LTGGNVFEYGVK 91
                                                                               96-506167/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatitis; cholangitis; cardiac allograft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 18.9%;
Similarity 27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610 AA;
                                                                                                   Innis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiac allograft rejection, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                   Zaror I;
                                                                                                                                                                                                                                                                                                                                                                      299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 298; DB 1; Le
Pred. No. 1.43e-20;
33; Mismatches 79;
                                   and decay accelerating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 610
                                                                                                                                                                                                                                                                                                                                                                                                                                            194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A portion (W06881) of the complement-inhibitor, decay accelerating factor (DAF), is used in novel chimeric proteins of formula A-R1-B-R2-C, where A and C are peptides (W06875-79, W06883-90) able to bind glycosaminoglycans (esp. heparin) present on cell surfaces, R1 is a portion of DAF or membrane co-factor protein (MCC, see also W06880), R2 is DAF when R1 is MCP or MCP when R1 is DAF, and B is a peptide that may have complement inhibitor activity. The chimeric proteins (see also W06882) are directed to cell surfaces where they inhibit complement-mediated cell lysis. They are used to treat and prevent disease states in which complement plays a role, e.g. sepsis, adult respiratory distress syndrome, reperfusion injury and the second complement in the second complement in the second complement plays a role, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human decay accelerating factor:
DAF; decay accelerating factor; human; C3 cc
retrovirus; vector; gene therapy; stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue damage
                                   This protein sequence comprises human decay accelerating factor (DAF), a protein that has C3 complement inhibitor activity. Claimed retroviral vector particles express a complement inhibitor such as DAF, and are thereby protected from inactivation upon exposure to body fluids containing complement. Also claimed are: (1) a producer cell producing the vector particle; and (2) a chimeric retroviral envelope protein (see also W26326) with at least part of the N-terminal receptor-binding domain removed and replaced by a protein domain having a complement inhibitor activity. The vector is used in a claimed method for transducing cells in the presence of a body fluid containing complement, preferably ex vivo, especially for gene therapy, e.g. of hereditary or acquired blood disorders by
                                                                                                                                                                                                                                                                                                Retroviral vector particle expressing complement inhibitor activity for transducing cells in body fluids containing complement Disclosure; Column 41-46; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
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21-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T84471
                        for gene therapy, e.g. of hereditary or actransduction of haematopoietic stem cells
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                                                                                                                                                                                                                                                                                                                                                                                                              Mason JM,
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(ALEX-) ALEXION PHARM INC.
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les 58; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNNDEGEWSGPPPEC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F--CKKKSCPNPGEIRNGQIDVPGG-IL-FGATISFSCNTGYKLFGSTSSFCLISGSSVQ 154
                                                                                                                                                                                                                                                                                                                                                                                          97-350243/32.
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    381 AA;
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larity 29.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Mat_protein
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factor; human; C3_complement inhibitor;
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Pred. No. 4.96e-20;
43; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 299;
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RESULT AND COLOR OF PRACTICAL PRACTI
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Best Local Similarity 29.7%;
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Best Local
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20-DEC-1994.
02-MAY-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Decay accelerating factor; DAF; mDAF; fusion protein; liposome; cell targeting; glycophosphatidylinositol; GPI; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig. 1a-1f; 36pp; English.

A probe (given in Q79865) based on the N-terminal sequence of human decay accelerating factor (DAF) was used to screen a HeLa cell lambda cDNA library. Isolated clones encoding membrane-bound DAF (mDAF) were obtained, and the full sequence of mDAF cDNA was determined (Q79863). The GPI signal domain of mDAF may be fised to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q79863.
Liposome(s) for targetting particular cells contg. fusion protein of glyco:phosphatidyl:inositol anchor and heterologous targetting protein, e.g. for delivering toxins to infected or
                                                                                                                                                                                                                                                                                                                                                                                                                                                 a heterologous protein and targeted to cell membrane surfaces sequence 381\ \text{AA};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caras IW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-1986; US-859107.
06-AUG-1987; US-083757.
19-DEC-1991; US-811048.
12-FEB-1993; US-017934.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 F--CKKKSCPNPGEIRNGQIDVPGG-IL-FGATISFSCNTGYKLFGSTSSFCLISGSSVQ 212
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213 WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 268
                                                                                                                                                                                                                                                     98 C-EVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVE 156
                                                                                                                                                                                                                                                                                                                     Local Similarity nes 58; Conser
                                                            59 LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG- 115
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                                                                                                                         F--CKKKSCPNPGEIRNGQIDVPGG-IL-FGATISFSCNTGYKLFGSTSSFCLISGSSVQ 212
                                                                                                                                                                                        CNELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRSLGNVI--MVC-RKGEWVALNP 58
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derivatization site"
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                                                                                                                                                                                                                                                                                                                                                   18.6%;
29.7%;
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Pred. No. 4.96e-20;
Micmatches 75;
                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                      Score 293; DB 1;
Pred. No. 4.96e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local
                                                                                                                                                                                                                                                                                         04-JUL-1990 (first entry)
Decay accelerating factor (DAF) of clones lambda 33 and lambda
DAF; allograft rejection; affinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       using recombinant DNA procedures.

Disclosure; Page 15-17; 20pp; English.
The probable phosphatidylinositol derivatisation site is Cys(330).
The DAF variant is useful for treating paraoxysmal nocturnal haemoglobinuria, or inflammatory or cell lytic autoimmune diseases. It may be used to ameliorate allograft rejection or autoimmune diseases. See also N70046, N70048.
                                         N-PSDB; N91043.
                                                                 WPI; 89-061177/08.
                                                                                                  Caras
                                                                                                                                                     09-FEB-1989.
3-AUG-1988; 02648.
6-AUG-1987; US-083757
                                                                                                                                                                                                                                                                                                                                                                                                                    /T 14
P94773 standard; protein; 381 AA.
                                                                                                                                                                                                                                            WÓ8901041-A.
                                                                                                                             GETH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New decay accelerating factor variants - obtained with the factor by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1987;
02-MAY-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
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Human decay acceleration factor variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 87-308481/44.
N-PSDB; N70047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP-244267-A.
04-NOV-1987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 --- DDGFWSKEKPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH) Genentech Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 268
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polypeptide for targeting protein to cell membrane
                                                                                                                       Genetech Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 18.6%;
Similarity 29.7%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303944.
US-859107.
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331. .347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 293; DB 1;
Pred. No. 4.96e-20;
43; Mismatches 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 381;
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                                                                                                                                                                                                                                                                                                           Example 3; Page 8-9; 15pp; Japanese.

This sequence is the human decay accelerating factor (DAF) protein.

DAF can be used in the viral vector of the invention. The viral vector contains a factor controlling the function of a human complement protein, particularly a membrane combining type protein. The viral vector, which is stable in situ, is useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Vector having complement controlling factor - useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1998.
15-MAY-1997; 125965.
15-MAY-1997; JP-125965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DINA-) DINABEKKU KENKYUSHO KK WPI; 99-074147/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral vector; ds.
   176
                                  269
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                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Decay accelerating factor protein.

DAF; decay accelerating factor; human; compliment protein; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1999 (first_entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W73505 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; 61pp; English.

Recombinant DAF's are useful in treatment of inflamatory or cell lytic autoimmune diseases and allograft rejection. Useful in diagnostic compositions or in affinity purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprisesphospholipid anchor domain with heterologous polypeptide.
                                                                                                                                                                                                                                                   Local Similarity 29.7%; hes 58; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKJEGDEEMHCS
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                                                                                      WSDPLPECREIYCPAPPQIDNG-IIQG--ERDH-YGYRQSVTYACNKGFTMIGEHSIYCT 268
                                                                                                                                           C-EVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVE
                              VNNDEGEWSGPPPEC 283
                                                           WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS
                                                                                                                          LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YR-ECDTDG-
---DDGFWSKEKPKC 187
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ilarity 29.7%;
Conservative
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                                                                                                                                                                                                                                                                        Score 293; DB 1;
Pred. No. 4.96e-20;
                                                                                                                                                                                                                                                        43; Mismatches
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Pred. No. 4.96e-20;
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Search completed: Thu Jun 8 21:37:19 2000 Job time: 11 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:40:50 2000; MasPar time 9.79 Seconds 641.132 Million cell updates/sec

Tabular output not generated.

Title: >US-09-316-163-10
Description: (1-265) from US09316163.pep
Perfect Score: 2029\_\_\_\_\_\_\_

Sequence: 1 EDCNELPPRRNTEILTGSWS.....EKSCDNPYIPNGDYSPLRIK 265

Scoring table: PAM 150 Gap 11

Searched: 188963 segs, 23686106 residues
Post-processing: Minimum Match 08
Listing first 45, Summaries

a Tgeneseq36

Database:

Statistics: Mean 32.240; Variance 119.188; scale 0.271

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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357	254	251	377	373	324	279	279	384	384	377	377	376	360	360	302	302	830	263	581	216	240	Length
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Human membrane cofacto	co-factor		CD46 from clone pm5.1.	clone	clone pm5	rane cotactor	protein SEQ ID	CD46.		•			Tulri	membrane	Saimiri S	secreted		quence or		PRRBUEH4 LO	partial Complem	Description
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18.3 263 1 P92003 Deduced sequence of co 6.80c-   371 18.3 263 1 P92003 Deduced sequence of co 6.80c-   372 18.3 263 1 P92003 Deduced sequence of co 6.80c-   374 17.0 830 1 R26320 Herpesvirus secreted g 1.19c-   374 16.8 302 1 R25793 Herpesvirus saimiri sC 1.19c-   375 16.8 360 1 W26319 Herpesvirus saimiri mC 1.19c-   376 1 R39331 CD46 wild-type.   5.29c-   5	1429 70.4 240 1 w39154 Human partial Compleme 1.09e- 1298 64.0 216 1 w39155 Clone prepriet 4.34e- 382 18.8 581 1 r3490 Human C4 binding prote 4.34e- 382 18.3 263 1 p92003 P-selectin. 344 17.0 830 1 R65216 P-selectin. 341 16.8 302 1 R55793 Herpesvirus saimiri sC 1.19e- 341 16.8 360 1 w26320 Herpesvirus saimiri sC 1.19e- 341 16.8 360 1 w26319 Herpesvirus saimiri mC 1.19e- 341 16.8 360 1 w26319 Herpesvirus saimiri mC 1.19e- 342 16.5 376 1 R93939 CD46 wild-type. 343 16.5 377 1 R93941 CD46 construct subscra 5.29e- 345 16.5 377 1 R10924 Human MCP. 346 1 R86316 Human MCP. 357 1 R10924 Human membrane cofactor 5.29e- 358 16.4 279 1 R41360 Membrane cofactor prot 8.68e- 358 16.4 377 1 R15233 CD46 from clone pm5.8 1.11e- 350 16.4 377 1 R15229 CD46 from clone pm5.6 1.11e- 350 16.3 254 1 R45361 Membrane cofactor prot 1.82e- 351 16.4 377 1 R10927 Human membrane cofactor prot 1.82e- 352 16.4 377 1 R10927 Human membrane cofactor prot 1.82e-

Db Qy Qy

121 INGSPISOKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNG 180

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	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.8	15.9	15.9	15.9	16.0	16.1	16.1	16.1	16.2	16.2	16.2	T0.7		7	16.2
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	Human complement type	CR1-4 (364-36/	-4 (250	-4 (309-370	-4 (SIGK, S	-4 (/81,	-4 (64K)	nce or	$\sim$	4 (99H, 1	(85R,	n beta-	Human beta-2 glycopro	Amino acid sequ	CD46 from clone		CRI protein	Human comprehenc recep		The principle of the contract		CD46 construct subSCR2	Human partial o
,	ent type	NAAH) a	717101		SIGN) did	/yD) anaro	analogue.	soluble co	analogue.	IUSE) anai	N) analo	Tycoprot	Тусоргос	sequence or	curd	יין ו		mc receb	10000	nence of	subSCR2	SubSCR2	compleme
	3.338-22	0.000	0. U.O. U.O.		3 530-33		2.700.22	3.036.22	1.000-12	1 600-00	1.036-22	1.03e-22	1 030-23	9. WO (I NO	0000		2 930-33	2.000-23	000-		. 33e-	2.33e-23	2.33e-23

### ALIGNMENTS

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PR 09-APR-1996; US-015083.

PR 06-MAR-1997; US-038614.

PA (BARD-) BARD DIAGNOSTIC SCI INC.

I Enfield DL, Hass GM, Kinders RJ;

RWPI; 97-512742/47.

Treating or free transparent of the control of the contr
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                                                                region
                                                                                                                          region
                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                   C4bp; monomer; complement protein; pJOD.C4bp.3; SCR; short consensus repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating or screening for cancer, e.g. renal or urogenital cancer-
by modulating or detecting tumour associated human complement Factor
H related antigen, or nucleic acid encoding it
Example 6B; Fig 6B; 104pp; English.
This partial protein is found in clone pRRB9FH410 and represents a
complement factor H related protein with homology to a region of the
human tumour-associated complement factor H (CFH). The detection of this
protein and a CFH antigen can be used in screening or for the treatment
of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer,
Agents that may modulate this antigen could be used in the manufacture of
a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                Human C4 binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R13490 standard; Protein; 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R13490;
                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-1991
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Clone pRRB9FH410 CFH related protein fragment.
Complement factor H; tumour associated antigen; renal cancer;
urogenital cancer; medicament; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIK 171
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16-OCT-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AVRFYCNSGYKIEGDEEMHCSDDGFWGKEKPKGVEISCKSPDVINGSPISQKIIYKENER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               medicament for L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 DYSPLRIK 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENER 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.08;
Similarity 99.48;
170; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                 /label- SCR7
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                         /label= SCR8
                                                                                                                                                /label= C4bp
                                                                                                                                                                                                    /label= signal_peptide
                                                             . 155
                                                                                                                                                                                  . 581
                                                                                                                       . 93
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Pred. No. 1.28e-132;
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DR N-EDB; 013042.

PT New C4 binding protein fusion proteins and DNA encoding them comprise assemblies of C4bp monomers linked to functional moiety, PT e.g. AZT, useful as delivery vehicles in diagnosis and therapy CC presence was deduced from human hepatocyte (Hep G2) cDNA CC obtained following PCR amplification. The protein is a monomer containing 8 SCRs. Each SCR forms a looped domain due to the presence of two intradomain disulphide bonds (only the disulphide cc bresence of two intradomain disulphide bonds (only the disulphide cc bresence of two intradomain disulphide bonds (only the disulphide cc bresence of two intradomain disulphide bonds (only the disulphide cc bresence of two intradomain disulphide bonds (only the disulphide cc bresence of two intradomain disulphide bonds (only the disulphide cc the first cysteine residue bonds with the fourth. This secondary structure is cresponsible for the conformational flexibility of the C4bp monomer. CC cysteine residue bonds with the fourth. This secondary structure is cresponsible for the conformational flexibility of the C4bp monomer. CC is fused to the C-terminal of a protein such as a viral receptor, cc cell ligand, a bacterial, viral or parasitic immunogen, enzyme, cc cytokine, toxin, etc. See also Q13243-51.
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P92003 standard; protein; 263 AA
                                                                                                                          248 SCDN-PYIPNG
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Pasek MP, Winkler G, Liu TR;
WPI; 91-252613/34.
                                                                                                                                                                               282 SCINLPDIPHA 292
                                                                                                                                                                                                                                                                                 222 TCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPSPPACEPN 281
                                                                                                                                                                                                                                                                                                                                              135 ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS-D-D--GFWSKEKPKCVEI
                                                                                                                                                                                                                                                                                                                                                                                               166 RNGR--HSG-E-ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 VEIKT-DL-SFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPDI 165
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26-JAN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 FILIGGNVFEYGVKAVYTCNEGYQLLGEINYR-EC-DTD-GWINDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTFCIY-KR-CRHPGELRNGQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 79; Conser
                                                                                                                                                                                                                          SCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEK
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ilarity 31.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-470888.
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65. .9;
/note=
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.e= "intradomain"
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el= SCR4
.406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 382; DB 1;
Pred. No. 4.34e-29;
52; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98;
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Best Local
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- encoded by Vaccinia virus 35K gene
Disclosure; Figure 2A, 20pp; English.
C4b-binding protein which specifically blocks human complement cascades.
It is the deduced sequence of a 35kDa protein encoded by sequence 52-840 of the 35K gene of vaccinia virus strain WR. Note a - these sites indicate the start of 60 amino acid tandem repeating units which have a consensus sequence. The signal peptide sequence is not found in purified 35K protein recovered from the medium of cells infected with vaccinia virus strain WR. A suggested use is to treat diseases due to abnormally had complement activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-1990 (first entry)
Deduced sequence of complement 4b (C4b) binding protein
Vaccinia virus WR strain; anti-complement protein; complement
inactivators; complement 4b; C4b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; N90113
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20-AUG-1988; 239208.
20-AUG-1988; US-239208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH) Nat Inst of Health.
Kotwal G;
                                                                                                           Control elements; gene expression; endothelial cells; megakaryocytes; rheumatoid arthritis; ischaemic injur atherosclerosis; bacterial sepsis; tumour metastases.
                                                                                                                                                           P-selectin
                                                                                                                                                                                                           R65216 standard; Protein; 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     high complement activity.
             02-MAR-1995.
19-AUG-1994; U09395.
20-AUG-1993; US-110158.
(OKLA ) UNIV OKLAHOMA STATE.
                                                                                                                                                                          04-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                          154
                                                                                                                                                                                                                                                                                                         208 HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC 261
                                                                                                                                                                                                                                                                                                                                         134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                         97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89-165451/22.
                                                                                                                                                                                                                                                                          SPDVINGSPISQ-KIIKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                        ISNGR--HNGYE-DF-YTDGSYVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP 207
                                                                                                                                                                                                                                                                                                                                                                                                        FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--WINDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                          LDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEPPISESVKCQSPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                             sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.3%;
llarity 33.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "See note a in comments below."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
37; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 371; DB 1; Pred. No. 6.80e-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 263;
                                                                                                                                 injury;
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              retroviral vector particle expressing complement inhibitor activity properties and complement inhibitor activity properties and complement inhibitor activity properties and complement inhibitor sequence comprises the herpesvirus Saimiri secreted complement sequence comprises the herpesvirus Saimiri secreted complement complement complement complement complement and complement and complement and complement are the protected from inactivation upon exposure to body fluids containing complement. Also claimed are: (1) a producer cell producing the vector particle; and (2) a chimeric complement are recomplement and complement complement and complement are retroviral envelope protein (see also W26324) with at least part complement inhibitor activity. The containing a complement inhibitor activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression control elements in the 5'- flanking region of the p-selectin gene - for regulating gene expression in endothelial cells and mega:karyocyte(s)
Disclosure; Fig 1; 88pp; English.
The sequence is that of the P-selectin gene product from endothelial cells, determined from a composite of four overlapping cDNAs: lambda GMPE1-lambda GMPE4. The P-selectin gene or its fragments may be used GMPE1-lambda GMPE4. The P-selectin gene or its fragments may be used
                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997.
21-JUL-1994;
21-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to inhibit P-selectin expression, thus controlling inflammatory and haemostatic processes in e.g. rheumatoid arthritis, ischaemic injury, bacterial sepsis, tumour metastases, atherosclerosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 95-106847/14
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                                                                                                                                                                                                                                                                               N-PSDB; T84474.
                                                                                                                                                                                                                                                                                               Mason JM, Squinto WPI; 97-350243/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpesvirus secreted
                                                                                                                                                                                                                                                                                                                                     (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 ECGELELPQHV-LMNCSHPLGNFSFNSQCSFHCTDGYQVNGPSKLECLASGIWTN-KP-P 255
presence of a body fluid containing complement, preferably ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 APAPVCKAVQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 TESG-WR-PLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 DNLGQWTAPAPVCQALQCQDLPVPN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 GHWSAPLPTCEAISCEPLESPVHGSMDCSPSLRAFQYDTNCSFRCAEGFMLRG-ADIVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 17.0%;
Local Similarity 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFWSKEKPKCVEISCKSPDV-INGS-PISQKI-IYKENERFQYKCNMGYEYSERGDAV-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
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830 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rus secreted glycoprotein sCCPH. complement inhibitor; retroviru
                                                                                                                                                                                                                                                                                                                Squinto SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                           US-278630
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 344; DB 1; Length 830; Pred. No. 5.67e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retrovirus; vector; gene therapy;
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Disclosure; Page 37-39; 59pp; English.

Gene sequences for 3 complement regulatory proteins encoded within the genome of herpesvirus Saimiri (HVS) are disclosed, i.e. membrane complement control protein homolog (mCCPH) (Q66956), secreted complement control protein homolog (seCPH) (Q66957) and HVS-15 (Q66958). mCCPH and sCCPH share substantial homology with the human complement inhibitory proteins factor H, CD35, CD46, CD55 and C4bp, which inhibit C3 convertase activity in the complement cascade. The gene sequences and corresponding proteins (R55792-94) can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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New complement regulatory proteins of Herpes virus Saimiri - are used to inhibit complement-mediated lysis in treating immune
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12-JAN-1993; U00672.
12-JAN-1993; WO-U00672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sCCPH; secreted complement control protein homolog; mCCPH; membrane complement control protein homolog; HVS-15;
156 GTHINVK-DF-YTYLDTVTYSCNDETKLTLIGPSSKLCSETGSWVPNGETKCEFIFCKLP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement regulatory protein; complement inhibitory protein.
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Herpesvirus saimiri sCCPH.
                                                                                                                                    100 NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
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                                                                                                                                                                                                                                                                      44 YPNGTTLHVTCREGYAKRPVQTVTCVNGNW-TV-P-KKCQKKKCSTPQDLLNGRYTVTG- 99
                                                                                                                                                                                                          24 YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG 83
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                                                                                                                                                                                                                                                                                                                                                                                      h 16.8%;
Similarity 31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the complement arm of the immune system. e 302 AA;
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Pred. No. 1.19e-24;
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Pred. No. 1.19e-24;
45; Mismatches 91
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                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 302;
                                                                                                                                                                                                                                                                                                                                            91; Indels 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT Retroviral vector particle expressing complement inhibitor activity PT for transducing cells in body fluids containing complement Disclosure; Column 50-52; 32pp; English.

CC This protein sequence comprises the herpesvirus Saimiri membrane CC glycoprotein mcCPH, an inhibitor of complement inhibitor such as CCPH, and are thus protected from inactivation upon exposure to CC producer cell producing the vector particle; and (2) a chimeric CC producer cell producing the vector particle; and (2) a chimeric CC retroviral envelope protein (see also W26324) with at least part CC of the N-terminal receptor-binding domain removed and replaced by CC aprotein domain having a complement inhibitor activity. The CC prosence of a body fluid containing complement, preferably ex vivo, CC especially for gene therapy, e.g. of hereditary or acquired blood CC disorders by transduction of haematopoletic stem cells.
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22-FEB-1995 (first entry)
                   R55792;
                                     R55792 standard; Protein;
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21-JUL-1994; US-2780
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W26319 standard;
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les 74; Conserv
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                                                                                                                                                                           IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP
                                                                                                                                                                                                                                                   NVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG---WTNDIPICEVVKCLPVTAPENGK 138
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21. .360
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Pred. No. 1.19e-24
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12-JAN-1993; WO-U00672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD46; recombinant protein; short consensus repeat; SCR; regulator of complement activation; transgenic animal; pig;
Disclosure; Page 32-33; 60pp; E
A cDNA sequence (T17595) codes
                                                                                                   Increasing prodn. of recombinant proteins,
the amt. of A and/or T in an A and/or T ri
                                                                                                                                                                                                                       30-AUG-1995; AU0553.
30-AUG-1994; AU-007724.
(AUST-) AUSTIN RES INST
Christiansen D, Lovela
                                                                                                                                                                                                                                                                                                                                                                                  WO9606937-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organ transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD46 wild-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R93939 standard; Protein; 376
                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 DVING-SPISQKIIYHENERFQYKCNMGYE-YSERGDAVCTESGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 YPNGTTLHVTCREGYAKRPVQTVTCVNGNW-TV-P-KKCQKKKCSTPQDLLNGRYTVTG- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 16.8%; Jocal Similarity 31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement regulatory proteins of Herpes virus Saimiri - are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94-249210/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTHTNVK-DF-YTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVFEYGVKAVYTCNEGYQLLGEINYREC - - DTDG - - - WTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 ĀA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fleckenstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                          Loveland B, McKenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 341; DB 1;
Pred. No. 1.19e-24;
         English.
s for wild-type CD46 (R93939), a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                         rich
                                                                                                   esp. CD46 - by reducing th region of encoding ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                      DE RESERVATION OF THE PROPERTY OF THE PROPERTY
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   Matches
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-1996.
30-AUG-1995; AU0553.
30-AUG-1994; AU-007724.
(AUST-) AUSTIN RES INST.
Christiansen D, Loveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulator of complement activation. Expression of CD46 in eukaryotic host cells, e.g. COS-7 and CHO-KL, is facilitated by lowering the A+T content of the short consensus repeat regions of the CD46 gene (see T17596-99) to give products (R93940-43) useful e.g. as immunomodulators. Modified CD46 may also be expressed on the organs of transgenic animals of use for organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transplantation
                                                                                                                                                                                     Claim 12; Page 36-37; 60pp; English.

CD46 subSCR3 (R93941) is the product of a cDNA construct
(R17597) obtd by splice overlap extension PCR of wild type CD46
(CDNA (T17595). The A+T content of AT-rich exon 5 of the CD46
gene, encoding the short consensus repeat 3 (SCR3) region of
CD46, is lowered. This results in improved prodn. in eukaryotic
host cells, e.g. CHO-K1 and COS-7. CD46 subSCR3 is used to prevent
complement or inflammation-mediated tissue damage, to improve
immunity to tumours or viruses, to control fertilisation and to
prevent spontaneous abortion. Expression in transgenic animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD46; recombinant protein; short consensus repeat; regulator of complement activation; transgenic anim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R93941;
21-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organ transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD46 construct subSCR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R93941 standard; Protein; 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing prodn. of recombinant proteins, esp. CD46 - by reducing the amt. of A and/or T in an A and/or T rich region of encoding ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T17597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9606937-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 DGSDTIVCDSNSTWDPPVPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 -WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGD
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
Local Similarity es 81; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MYC-RKGEWVALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-DACYRETCPYIRD-PLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYYKATVMFE--CDKGF-YL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERGDA-VC-TESGW-RPLPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96-160368/16.
                                                                                                                                                                      pigs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 AA;
                                                                                                                                   provides organs suitable for transplantation. 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loveland B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.5%;
                                   16.5%;
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Pred. No. 5.29e-24;
   Score 335; DB 1;
Pred. No. 5.29e-24;
54; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McKenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milland
                                                                          Length 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               animal; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 27;
                 Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                 Gaps
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33 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90

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RESULT I DA ACC WITH 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y Surfaces which prevent or reduce complement activation - having surface bound homologous complement restriction factor Example 1; Fig 1A; 50pp; English.

C The present sequence is human MCP, which was used in the development of a novel surface bound to a homologous complement crestriction factor (HCRF), where the surface is not a surface to which HCRF binds in vivo. The surface can be used in medical caparatus (e.g. extra-corporeal circulation systems, tubing, valves, membranes, pumps, oxygenators, catheters, cannulas, fluid creservoirs or prostheses), medical dressings, surgical equipment, can abnormality which prevents the complement spatient has commandly or from being properly regulated) and purification can be used to reduce or prevent activation of complement, and to sequence morbidity due to complement activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
116 -WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 97-489571/45.
N-PSDB; T90306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; MCP; surface; homologous complement restriction factor; HCRF; medical apparatus; medical dressing; surgical equipment; diagnostic kit; prevention; purification device; reduction; complement activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watkins NJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1996;
28-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                   33 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90
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                                                                                                                                   PLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG 115
                                                                                                                                                                                               D-DACYRETCPYIRD-PLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVA 148
                                                                                                                                                                                                                                                                      EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MVC-RKGEWVALN 57
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 335; DB 1;
Pred. No. 5.29e-24;
54; Mismatches 99
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant mammalian membrane co-factor protein - for treating diseases with altered complement activity e.g. inflammatory and auto-immune conditions
Disclosure; fig 1, 38pp; English.
This human isoform of a membrane cofactor protein (MCP) is useful in a pharmaceutical compsn. for the treatment of inflammatory and autoimmune diseases mediated by excess or misdirection of complement activity e.g. rheumatoid arthritis or multiple sclerosis. Protection against tissue injury caused by e.g. myocardial infarction or stroke may also be provided. Antibodies raised farction or stroke may also be provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against this MCP can be used in autoimmune disease diagnosis to predict the probability of recurrent miscarriages by testing for MCP levels in the placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also Q10865-66 and R10927.
170 EEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYEYS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q10864
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19-APR-1990; US-510709.
(UNIW ) UNIV OF WASHINGTON.
                                                       206 STIYCGDNSYWSRAAPECKYYKCRFPYYENGKQISGFGKKFYYKATYMFE--CDKGF-YL 262
                                                                                                                     116 -WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Atkinson JP;
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20-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
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                                                                                                                                                                                                                                                                    58
                                                                                                                                                                                                                                                                                                        91 D-DACYRETCPYIRD-PLNGQAVFANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                33 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 EEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERPQYKCNMGYEYS 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                   IWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGE 205
                                                                                                                                                                                                                                                PLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG 115
                                                                                                                                                                                                                                                                                                                                                                         EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MVC-RKGEWVALN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CYT2 cytoplasmic tail region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= unknown
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31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 335; DB 1;
Pred. No. 5.29e-24;
54; Mismatches 99
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ERGDA-VC-TESGW-RPLPSC DGSDTIVCDSNSTWDPPVPKC

244 283

R86316; 15-APR-1996

(first

entry)

Human CD46.

R86316 standard; Protein; 384

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terminal complement inhibitor chimeric protein and nucleic acid esp. against human complement, useful for protecting cells from complement attack e.g. in organ transplantation

Disclosure; Page 66-68; 85pp; English.

A terminal complement inhibitor protein (CIP), is used in the romatruction of chimeric cDNA coding for transmembrane terminal CIP, pref. comprising amino acids 1-77 of CD59 fused to amino acids 270-350 (the transmembrane domain) of CD46 (R86316). Such chimeric cDNA is incorporated into a retrovirus vector and used in the breeding of transgenic animals as a means of producing transgenic organs that are protected against human complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terminal complement inhibitor protein; terminal CIP; CD59; CD46; transmembrane terminal CIP; TMTCIP; Ly6 antigen; transgenic animal; organ transplantation; glycosyl-phosphatidylinositol; GPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALEX-) ALEXION PHARM INC. Rollins S, Rother RP, Sc WPI; 95-320335/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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03-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    attack upon
                              09-NOV-1998 (first entry)
rsMCP protein SEQ ID NO:25 from WO9829453 Claim 14.
Drug; cell membrane-directed drug; phospholipid; lipid bilayer;
                                                                                  W69523 standard; peptide; W69523;
Synthetic
                 cell cortex; blood
                                                                                                                                                                                                                                         170 EEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYEYS
                                                                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                       263 DGSDTIVCDSNSTWDPPVPKC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90
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                                                                                                                                                                                                                                                                                                                                        IWSGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGE 205
                                                                                                                                                                                                                                                                                                                                                                             PLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MVC-RKGEWVALN 57
                                                                                                                                                                        ERGDA-VC-TESGW-RPLPSC 244
                                                                                                                                                                                                                                                                         STIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYYKATVMFE--CDKGF-YL 262
                                                                                                                                                                                                                                                                                                           -WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplantation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.5%;
                 coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Squinto SP;
                                                                                                      279 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 335; DB 1; 1
Pred. No. 5.29e-24;
54; Mismatches 99
                   inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99;
                 immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                     disorder
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Search completed: Thu

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                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes drug compositions which contain as can active component a peptide which has specific affinity to particular cphospholipids (such as phosphatidyl ethanolamine or phosphatidyl serine). CC especially to phospholipids which constitute a lipid bilayer of cellular cortex and of which the concentration in the bilayer increases in cells which are abnormal (e.g. through injury, denaturation or activation). In CC which are abnormal (e.g. through injury, denaturation or activation). In CC particular, the peptide contains a sequence having phospholipid affinity CC and a structure of formula (I): (Al)a-(A2)b-(A3)c, where (Al) is one of two specific sequences (see W69516 and W69517) or MEVIGCEAQNIX (see CC TRYLRIHPOSWYHQIALR, LRYLRIHPOSWYHQIALR (see W69517) or MEVIGCEAQNIX (see CC W69518); a = 0-5; b = 1-5, and c = 0-5, preferred are the formulae CC W69518); a = 0-5; b = 1-5, and c = 0-5, preferred are the formulae CC M2-A2-A3, A2-A3, A2-A3, a2-A2-A3, and A2-A3 (especially A2-A3, A2-A3, accordance is linked to a peptide such as a blood factor, especially thrombo-modulin, urina-statin or membrane CC cofactor protein. The drugs are used for the treatment and prevention of CC diseases involving blood coagulation, inflammatory and immunological constraints. The present sequence represents a peptide from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drugs containing peptide(s) with specific affinity to phospholipid(s) - such as phosphatidyl serine, for treatment of blood coagulation, inflammatory and immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-1998.
05-JAN-1998; J00002.
27-DEC-1996; JP-359053
(MOCH ) MOCHIDA PHARM (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             blood coagulation, inflammatory and immunological disorders Claim 14; Page 81-83; 117pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 98-388051/33.
N-PSDB; V40047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hasegawa T, Kuriyama S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9829453-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
                                                                                            172
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    229
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                                                                                                                                                                                                                                                                                                                     58
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                                                                                                                                                                                                                                                                                                                                                                                                               1 CEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVSD-
                                                                                                                                                                                                                                                                                                                 DACYRETCPYIRD-PLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIW 116
                                                                                                                                    IYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYYKATVMFE--CDKGF-YLDG
                                                                                                                                                                                                                                                                                                                                                                CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNV-I-MVC-RKGEWVALNPL 59
                                                                                         MHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYEYSER
                                                                                                                                                                                 TNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCN-S-G---YKIEGDEE
                                                                                                                                                                                                                           SGKPPICEKVLCTPPPKIKNGKHTFSEVEV-FEY-L-DAVTYSCDPAPGPDPFSLIGEST
                                                                                                                                                                                                                                                                           RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGE-INYRE-CDTDG-W
    GDA-VC-TESGW-RPLPSCEEKSCDNPYIPN-GDYS
                                            SDTIVCDSNSTWDPPVPKCL-KGPRPTYKPPVSNYP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 333; DB 1;
Pred. No. 8.68e-24;
57; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 105;
         260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jun 8 21:41:21 2000; MasPar time 16.86 Seconds 741.518 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-316-163-10 (1-265) from US09316163.pep 2029

Sequence: 1 EDCNELPPRRNTEILTGSWS.....EKSCDNPYIPNGDYSPLRIK 265

Scoring table: PAM 150 Gap 11

142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Lighting figst 45 summaries

Database:

Statistics: Mean 43.012; Variance 68.118; scale 0.631

1:pird 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query Match	Length	BG	ID	Description	Pred. No.
1	2029	100.0	449	$\vdash$	NBHUHS	complement factor H p	0.00e+00
2	2029	100.0	1231	Н	NBHUH		0.00e+00
ω	1439	70.9	1234	Н	NBMSH	nt factor H	0.00e+00
4	952	46.9	669	2	865551	factor H - bovine (ir	9.39e-211
տ	587	28.9	1053	N	S46199	probable complement r	3.83e-IIb
σ	406	20.0	597	ш	S53711	C4BP alpha chain prec	. Lie-/
7	388	19.1	263	ب	WMVZSP	apolipoprotein H homo	
œ	382	18.8	597	_	NBHUC4	C4b-binding protein a	. 000
9	371	18.3	345	Н	NBMS		.20e-6
10	371	18.3	558	2	S57953		ď
11	357	17.6	263	Ь	C36838	complement control pr	1.05e-58
12	353	17.4	560	N	T16833	hypothetical protein	9.926-58
13	344	17.0	830	N	A30359	P-selectin precursor	1.496-55
14	341	16.8	302	ب	WMBE1E	secretory complement	1 . aaa aa
15	341	16.8	360	Ц	WMBE2E		7.000.00
16	341	16.8	469	ب	NBMSC4	9	7.886-00
17	341	16.8	768	ນ	153821	,	7.88e-00
18	338	16.7	349	N	G02913	sperm CD46 - numan (1	# . LOC - L#
19	338	16.7	369	N	I57998	н	4.100-54
20	338	16.7	610	,_	146001	C4b-binding protein a	4. LOC - C4
21	339	16.7	768	N	A42755	P-selectin precursor	2.096-04
22	334	16.5	345	ш	NBBO	apolipoprotein H prec	3.82e-03
23	335	16.5	377	Ν	154479	membrane colactor pro	V. 136.77

## ALIGNMENTS

#cross·referent #accession #molecule. ##molecule. ##residues ##note	REFERENCE #authors #journal #title	##status ##molecule_type ##residues ##note	#authors #journal #title #cross-referent	#cross-references MUID: #accession \$03013 ##molecule_type mRNA ##residues 1-44 ##cross-references E ##note part ##note 402-	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors #Journal #title
containing the binding site for C3b.  nces MUID:87054207  A27877  -type mRNA 'IL',55-401,'Y',403-449 ##label SCH an additional nucleotide present within t Glu-310 was thought to be a cloning art ignored in translation	A2/8/, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Schulz, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Dierich, M.P.  Bur. J. Immunol. (1986) 16:1351-1355  Bur. J. Immunol. (1986) 16:1351-1355  Human complement factor H: isolation of cDNA clones and partial cONA sequence of the 38-kDa tryptic fragment	not compared with conceptual translation  type mRNA 1-33;434-449 ##label EST only portions of this 1.8 kilobase mRNA were sequenced	ACCESSION REALES AND ACCESSION RESEARCH SENDERS AND ACCESSION R6028	#cross-references MUID:88134059  #accession S03013  ##molecule_type mRNA ##residues 1-449 ##label RIP ##cross-references EMBL:X07523; EMBL:Y00716; NID:g32492; ##cross-references EMBL:X07523; EMBL:Y00716; NID:g32492; ##note pIDN:CAA30403.1; PID:g758073  ##note mature protein was confirmed by protein sequencing ##note 402-Tyr was also found	NBHUHS #type complete complement factor H precursor, short splice form - human complement factor H-related protein; complement protein H formal_name Homo sapiens #common_name man #formal_name Homo sapiens #common_name man #common_name man #formal_name Homo sapiens #common_name man #formal_name Homo sapiens #common_name man #formal_name Homo sapiens #formal_name #formal_name Homo sapiens #formal_name man #formal_name man #formal_name #formal_name man #formal_name #formal_name #formal_name human formal_name #formal_name human formal_name human form

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CLASSIFICATION
                                                                                                                FEATURE
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                                                                                                                                                                                                                                                                                                                                              FUNCTION
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         21-80
                                                                     19-449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##CIOSS-references GDB:120041; OMIM:134370 #map_position 1q32-1q32 UETICS HF2
                                                                                                                                                                                                                             #pathway
                                                                                                                                                                                                                                                                                                                      #description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.;
Pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.
Biochemistry (1992) 31:3626-3634
#title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #title Purification and structural studies on the complement-system control protein beta-1-H (factor H).
#cross-references_MUID:83048213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 226-401,'Y',403-449 ##label KRI
##cross-references GB:M12383; NID:g180472; PIDN:AAA52013.1; PID:g180473
Factor H has also been found bound to cell membranes in an unknown
manner. However, it has at least one cell attachment site motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
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##moridines 27-76 ##label SC2
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##mesidues 19-20,'Q',22-29,'V',31-33,'Q',35 ##label SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in liver. See also PIR:NBHUH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in repeat 4.
                                                                                                                                                                                                        a cofactor in the inactivation of C3b by serine proteinase also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway complement alternate pathway
                                                                                                                                     alternative splicing; complement alternate pathway;
                                                                                                                                                                                  #superfamily complement factor H; complement factor H repeat
                                                                                                                                                                                                                                                                                                                                                                   the correspondence between the two loci and the sequences indicated is unclear; factor H has been reported to have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDB:HF2; HF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kristensen, T.; Wetsel, R.A.; Tack, B.F.
J. Immunol. (1986) 136:3407-3411
Structural analysis of human complement protein H: homology
with C4b binding protein, beta(2)-glycoprotein I, and the
Ba fragment of B.
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Biochem. J. (1982) 205:285-293
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Eur. J. Immunol. (1987) 17:1485-1489
Human complement factor H: expression of an additional truncated gene product of 43 kDa in human liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           annotation; NMR structure determination, residues 264-292
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                                                                                                                                glycoprotein; plasma
                                                                                                                                                                                                                                                                                                                                                          several allelic forms
                       #domain signal sequence #status predicted #label SIG\
#product complement factor H, short splice form #status
experimental #label MAT\
    #domain complement factor H repeat homology #label FH01\
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##molecule_type mRNA
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#cross-references MUID:91184292
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178-205,210-251,
237-262,267-309,
294-320,325-374,
357-385,389-431,
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                                                                                                                                                                                                     259 LPSCEEKSCDNPYIPNGDYSPLRIK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 LPSCEEKSCDNPYIPNGDYSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 PICEVVKCLPYTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 KCOKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 78
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Similarity 100.0%;
                                                                      Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.
Eur. J. Immunol. (1991) 21:799-802
Human complement factor H: two factor H proteins are derived,
from alternatively spliced transcripts.
                                 A60238
                                                                                                                                                                                                                                                                                                                                                                                   S00254
                                                                                                                                                                                                                                                                                                                                                                                                                                         The complete amino acid sequence of human complement factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B Biochem. J. (1988) 249:593-602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBHUH #type complete complement factor H precursor, long splice form - human formal_name Homo sapiens #common_name man 31_Dec-1993_#sequence_revision 31-Dec-1993 #text_change
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not compared with conceptual translation
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complement factor H repeat homology #label complement factor H repeat homology #label complement factor H repeat homology #label complement factor H repeat homology #label
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Pred. No. 0.00e+00;
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#title Partial characterization of human complement factor H by protein and cDNA sequencing: homology with other complement ecross-references MUID:86188123
#accession A61565
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#title Sequence analysis of a cDNA clone encoding the C-terminal end of human complement factor H.
#cross-references MUID:88025472
#accession A54726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Sim, R.B.; Discipio, R.G.
#journal Biochem. J. (1982) 205:285-293
#title Purification and structural studies on the complement-system
control protein beta-1-H (factor H).
#cross-references_MUID:83048213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.;

pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.

#journal Biochemistry (1992) 31:3626-363

Biochemistry Gipel Structure of the fifth repeat of factor H: A second example of the complement control protein module.

#cross-references MUID:92232649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #title Three-dimensional structure of a complement control protein module in solution.
#cross-references MUID:91278097
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                                                                                                                                                          ##molecule_type mRNA*
##residues 1047-1231 ##label RES
##cross-references GB:M65294; NID:g183766; PIDN:AAA35948.1; PID:g183767
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                                                                                                                                                                                                                                                                                                                     J. Immunol. (1991) 146:3190-3196 (Cloning of the 1.4-kb mRNA species of human complement factor H reveals a novel member of the short consensus repeat family related to the carboxy terminal of the classical 150-kDa molecule.
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                       Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano, A.; Gordon, D.L.; Burns, G.F.
Biochim. Blophys. Acta (1996) 1289;305-311
Factor H co-purifies with thrombospondin isolated from
                                                                                                                                                                                                                                                                            172654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Estaller, C.; Koistinen, V.; Schwaeble, W.; Dierich, M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation; NMR structure determination, residues 264-292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation; NMR structure determination, residues 927-985
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platelet secretate.
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GENETICS
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                                                            536-564,569-611,
597-623,630-673,
659-684,691-733,
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691-744
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325-385
389-442
448-505
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#map_position 1q32-1q32
the correspondence between the two loci and the sequences
#note indicated is unclear; factor H has been reported to have
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210-262
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781-803,811-853,
839-864,870-915,
901-926,931-973,
                                                719-744,753-792,
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##residues 411-419;574-578,580-582 ##label CAR
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experimental #label MAT\
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#product complement factor H #status experimental #label
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#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04\
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#authors
                                                                                                                                                       #authors Natsuume-Bakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y.
#journal J. Immunol. (1990) 144:358-362
#title Demonstration of an unusual allelic variation of mouse factor
#toross-references MUD:90111033
#cross-references MUD:90111033
                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors
#journal
                                                                                                                                                                                                                                                                                                                                                                #authors Kristensen, T.; Tack, B.F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3963-3967
#title Murine protein H is comprised of 20 repeating units, 61 amino acids in length.
#cross-references MUID:86233353
#cross-references MUID:86233353
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                                             ##residues 1-18 ##label RES ##cross-references GB:M31979; NID:g193726; PIDN:AAA37762.1; PID:g193729
                                                                                              ##molecule_type mRNA
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##residues 1-1234 ##label KRI
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Similarity 100.0%;
265; Conservative
          Munoz-Canoves, P.; Tack, B.F.; Vik, D.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement factor H precursor - mouse protein beta-1-H protein beta-1-H formal_name Mus musculus #common_name house mouse 30.Sep-1987 #sequence_revision 30-Sep-1987 #text_change
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536-564,569-610,
597-622,629-672,
658-683,690-732,
718-743,752-791,
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178-205,210-251,

237-262,267-309,

294-320,325-374,

357-385,389-431,

416-442,448-494,
                                                                                                1053-1096,
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11143-1168,
                                  676,721,773,801,
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906-931,936-978,
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##cross references GB.J02891; NID:g193805; PIDN:AAA37795.1; PID:g553926
NT Two codominant alleles of factor H are present in mice.
NT Factor H functions as a cofactor in the inactivation of C3b by serine proteinase I and also increases the rate of dissociation of the C3bbb complex (C3 convertase) and the (C3b)nBb complex (C5
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Analysis of complement factor H mRNA expression:
Dexamethasone and IFN-gamma increase the level of H in L
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Query Match

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    187 RP 188
                                                                                                                  140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
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Local Similarity 67.0%;
                                     200 GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDY 259
                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                  LAEGNQFEYGAKVVYTCDEGYQMYGEMNFRECDTNGWTNDIPICEVVKCLPVTEPENGKI 66
                                                                            GQAVLPKATYKQNERVQYRCAAGFEYGQRGDTVCTKSGWTPAPTCIEITCDPPRIPNGVY 186
                                                                                                                                                         FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPPVILN 126
                                                                                                                                                                                                   LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                       h 46.9%;
Similarity 64.3%;
117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor H - bovine (fragment)
#formal_name Bos primigenius taurus #common_name cattle
19-Nar-1997 #sequence_revision 25-Apr-1997 #text_change
13-Aug-1999
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Pred. No. 0.00e+00;
39; Mismatches 48
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Pred. No. 9.39e-211;
29; Mismatches 36:
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#journal Biochem. J. (1994) 301:391-397
#title Cloning and characterization of a cDNA representing a putative complement-regulatory plasma protein from sand bass (Parablax neblifer).
#cross-references_MUID:94318039
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##residues 526-532,'X',534-537;809-817,'X',819-826 ##label
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                                                                                                                                                                       257 GDYSP 261
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                                                                                                                                                                                                                                                                                                                        141 SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN
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                                                                                                                                                                                                           279 TRYEP 283
                                                                                                                                                                                                                                                                                                                                                                                                  81
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                                                                                                                                                                                                                                                                                                                                                            IGG--PE-EATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
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Similarity 37.1%;
91; Conservation
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Pred. No. 3.83e-116;
41; Mismatches 101;
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                                                                                                                                                                                                    #authors Kotwal, G.J.; Moss, B.
#journal Nature (1988) 335:176-178
#title Vaccinia virus encodes a secretory polypeptide structurally
#cross-references MUD:88318974
#cross-references MUD:88318974
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174-234
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                                                                  ##experimental_source strain WR
                                                                                                                                          ##molecule_type DNA
                                                                                               ##residues 1-263 ##label KOT
##cross-references GB:X13166; NID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 KSC-DNPYIPNG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 NSCLGLPNVPHA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 IINGK-HNGGNE-DIH-TYGSSVTYSCNPRFSLLGEASISCTVKNKTVGVWSPSPPVCKE 236
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FICATION #superfamily C4b-binding protein alpha chain; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTNDIPICEVVKCLPVTA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 20.0%;
Similarity 32.9%;
           Goebel, S.J.; Johnson, G.P.; Perkus,
                                                 A4250:
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apolipoprotein H homolog precursor - vaccinia virus
35K secretory protein; C3L protein; virokine
#formal_name vaccinia virus
                                                                                                                                                                                   A31005
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#length 597
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Biochim. Biophys. Acta (1995) 1261:285-289
cDNA structure of rabbit C4b-binding protein alpha-chain.
Preserved sequence motive in complement regulatory protein modules which bind C4b.
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                                                                                         NID: g60690; PIDN: CAA31564.1;
        м. E.;
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homology #label FH2\
homology #label FH3\
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86-143
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Query Match 19.18;
Best Local Similarity 34.28;
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                                                                                ##molecule_type mRNA
##residues 1-597 ##label MA1
##cross-references GB:M31452; NID:g1905
##note the authors translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 ISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP 207
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##cross-references GB:M35027; NID
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                                                                                                                                                                                                                                                     Matsuguchi, T.; Okamura, S.; Aso, T.; Sata, T.; Niho, Y. Biochem. Biophys. Res. Commun. (1989) 165:138-144 Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein.
S02372
Lintin, S.J.; Lewin, A.R.; Reid, K.B.M
                                                                                                                                                                                                                      A33568
                                                                                                                                                                                                                                                                                                                                                                                                                                      A33568; S02372; A90326; A24182; A93134; S29492; A31785;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4b-binding protein alpha chain precursor - human C4BP; proline rich protein
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Virology (1990) 179:247-266
The complete DNA sequence of vaccinia virus
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Virology (1990) 179:517-563
Appendix to "The complete DNA sequence of vaccinia virus".
B42504
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#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH4
gth 263 #molecular-weight 28629 #checksum 8152
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#product C4b-binding protein homolog #status predicted
#label MAT\
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Pred. No. 2.94e-66;
37; Mismatches 96
                                                                                                                      NID:g190501;
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                                                                                      the codon GGA for residue 492 as
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#title Derivation of the sequence of the signal peptide in human
C4b-binding protein and interspecies cross-hybridisation of
the C4bp cDNA sequence.
#cross-references MUID:88242821
#accession S02372
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#title
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                                           #authors Suzuki, K.; Nishioka, J.
#journal J. Biol. Chem. (1988) 263:17034-17039
#title Binding Site for vitamin K-dependent protein S on complement
C4b-binding protein.
#cross-references MUID:89034204
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##cross-references EMBL:X07853
##note although the sequence determined extends to residue 9
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##residues 49-81 ##label CH1
##molecule_type protein
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Chung, L.P.; Bentley, D.R.; Reid, K.B.M.
Biochem. J. (1985) 230:133-141
Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.
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Mol. Immunol. (1985) 22:427-435
Amino acid sequence studies of human C4b-binding protein:
N-terminal sequence analysis and alignment of the fragments
produced by limited proteolysis with chymotrypsin and the
peptides produced by cyanogen bromide treatment.
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Structure of the gene coding for the alpha polypeptide chain of the human complement component C4b-binding protein.
                                                                                                                                                                                                                                                                                                                                       Hessing, M.; Kanters, D.; Takeya, H.; van't Veer, C.; Hackeng, T.M.; Iwanaga, S.; Bouma, B.N. FEBS Lett. (1993) 317.228-232
The region Ser(333)-Arg(356) of the alpha-chain of human C4b-binding protein is involved in the binding of complement C4b.
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                                                                                                                                                                                                         381-404 ##label HES
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1-597 ##label ASO

##cross-references GB.M62486; NID:g190498; PIDN:AAA36506.1; PID:g190500

##cross-references GB.M62486; NID:g190498; PIDN:AAA36506.1; PID:g1905000

##cross-references GB.M62486; NID:g190498; PIDN:AAA36506.1; PID:g190500

##cross-references GB.M62486; NID:g190498; PIDN:AAA3660.1; PID:g190500

##cross-references GB.M62486; PIDN:AAA3660.1; PID:g190500

##cross-references GB.M62486; PIDN:AAA3660.1; PID:g190500

##cross-references GB.M62486; PID:g190500

##cross-references GB.M62486; 
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#title
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Best Local
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484-538
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381-404
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175-234
239-294
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#map_position 1q32-1q32
#introns 48/1; 110/1; 143/2; 172/1; 236/1
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                                                                    67 TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTFCIY-KR-CRHPGELRNGQ 123
                                                                                                                                                 / Match 18.8%;
Local Similarity 31.5%;
nes 79; Conservative
20 SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
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#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
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#domain complement factor H repeat homology #label FH5\
#domain complement factor H repeat homology #label FH6\
#region complement factor H repeat homology #label FH7\
#domain complement factor H repeat homology #label FH7\
#domain complement factor H repeat homology #label FH7\
#domain complement factor H repeat homology #label FH8\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chylomicron; complement pathway; duplication;
                                                                                                                                                                                                                                                                                                               #molecular-weight 67033 #checksum 6374
                                                                                                                                                 Score 382; DB 1;
Pred. No. 8.65e-65;
52; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein alpha chain #status
                                                                                                                                                              98;
                                                                                                                                                                                                                                  Length 597
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                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                            (covalent)
                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                            #status
                                                                                                                                                              Gaps 20;
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γQ

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#map_position
CLASSIFICATION
                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                      GENETICS
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                                                                       205-260
264-325
23-66,51-79,84-124,
110-137,142-188,
174-200,205-248,
                                                                                                                                                                       20-345
23-79
                                                                                                                         142-200
                                                                                                                                                84-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitehead, A.S.

#journal Blochem. Blophys. Res. Commun. (1994) 200:1521-1528

#title Characterization, expression and evolution of mouse
beta2-glycoprotein I (apolipoprotein H).

#cross-references MUD:94242017
                                                                                                                                                                                                                                                                                                                                                                                               #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #cross-references MUID:92372000
                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-251,'R',253-345 ##label SEL ##cross-references GB:S70439; NID:g546780; PIDN:AAB30789.1; PID:g546781 ##experimental_source liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-252,'A',254-277,'N',279-345 ##label NON
##cross-references GB:D10056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 VEIKT-DL-SFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPDI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCDN-PYIPNG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCINLPDIPHA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPSPPACEPN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS-D-D--GFWSKEKPKCVEI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNGR--HSG-E-ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTLTGGNVFEYGVKAVMCCNEGYQLLGEINYR-EC-DTD-GWTNDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                             #superfamily apolipoprotein H; complement factor H repeat
                                                                                                                                                                                                                                                                                         chylomicron; duplication;
                                                                                                                                                                                                                                                                                                                                                                                       B2gp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sellar, G.C.; Steel, D.M.; Zafiropoulos, A.; Seery, L.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.; Natsuume-Sakai, S. Genomics (1992) 13:1082-1087 Molecular cloning of mouse beta-2-glycoprotein I and mapping of the gene to chromosome 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBMS #type complete
apolipoprotein H precursor - mouse
50K serum glycoprotein; activated protein C-binding protein;
beta-2-glycoprotein I
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A43286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Mus musculus #common_name house mouse
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
28_May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nonaka, M.; Matsuda, Y.; Shiroishi,
                                                                                                                                                                                                                                                                                                              homology
                                                                                                                                                                                                                                                                lipid binding; monomer;
                                                          #domain signal sequence #status predicted #label SIC\
#product applipoprotein H #status predicted #label MAT\
#domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH4\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the authors translated the codon ACT for residue 253 as Ala and ATG for residue 278 as Asn sequence extracted from NCBI backbone (NCBIN:111791, NCBIP:111794) and corrected to correspond with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide translation
                                                                                                                                                                                                                                                              glycoprotein;
plasma; VLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.; Moriwaki, K.; Nonaka
                                                                                                                                                                                                                                                                                  HDL; heparin binding;
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DЪ
                                                                                                                                                                                                                                                                                        SUMMARY
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REFERENCE
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                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                             15-72
77-134
139-199
204-258
263-324
328-386
390-443
447-501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.3%;
Best Local Similarity 29.4%;
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234-260,264-315,
300-307,325-345
105,117,162,183,
193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
32 YKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYG 89
                                                              43 YNCRPGYSRASSSQSLYCKPLGKW-QIN-IA-CVKKSCRNPGDLQNGKVEVKT-D-FLFG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references EMBL: Z50051; NID: g899379; PIDN: CAA90391.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 NG--S-PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSCDNPYI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 PNGD-YSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 KATVLYQGMRVK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK-SPDVI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 KDYRPSAGNNSLYQDTVVFKCLPHFAMIGNDTVMCTEQGNWTRL-PECLEVKCPFPPRPE 212
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 TYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 SYDPGEQIVYSCKPGYVSRGGMRRFTCPLTGMW-PINTLR-CVPRVCPFAGILENGIVRY 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGYVNYPAKPVLLYKDKATFG--CHETYKLDGPEEAECTKTGTWSFLPTCRE-SCKLPVK 269
                                                                                                                                      18.3%;
Similarity 30.5%;
73; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily C4b-binding protein alpha chain; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillarp, A.; Thern, A.; Dahlback, B. submitted to the EMBL Data Library, July 1995 Molecular cloning of rat C4b-binding protein alpha- and beta-chains: structural and functional relationships a
                                                                                                                                                                                                                                                                          #length 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $57953  #type complete
C4BP protein alpha chain precursor - rat
#formal_name Rattus norvegicus #common_name Norway rat
13-Jan-1996  #sequence_revision 01-Mar-1996  #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S57953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human, bovine, rabbit, mouse and rat proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-Aug-1999
                                                                                                                                                                                                                                                            #domain complement factor H repeat homology #label #domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-558 ##label HIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #disulfide_bonds #status predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted
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                                                                                                                                      Score 371; DB 2;
Pred. No. 4.20e-62;
57; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 371; DB 1; Length 345; Pred. No. 4.20e-62; 49; Mismatches 110; Indels
                                                                                                                                      Mismatches 87; Indels 22;
                                                                                                                                                                                                     Length 558;
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##status preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 PHPTILNGYLSSGFKRSYSYNDNVDFTCKYGYKLSGSSSSTCSPGNTWQPELPKC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 APENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 IS-NGR--HNGYN-DF-YIDGSVVTYSCNSGYSLIGNSGVLCSGGE-WSNP-PTCQIVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-263 ##label BLI
##cross-references GB:X69198; NID:g456758; PIDN:CAA48953.1; PID:g297195
FICATION #superfamily herpesvirus complement control protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 PISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRPLPSCEEKSC-DNPYIPNG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 INSGFKHTYKYKDSVRFVCQKGFVLRGSGVIHCEADGSWSPVPVCELNSCTDIPDIPNA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 PDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD--GFWSKEKPKCVEISCKSPDVINGS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 17.6%;
Local Similarity 33.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTLIGGNVFEYGVKAVYTCNEGYQLLGEIN-Y-RECDTDG--WINDIPICEVVKC-LPVT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDI-GG-V-DFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEF-FTYRSSVTYKCDPDFTLLGNASITCTVVNKTVGVWSPSPPTCERIICPWPKVLHGT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKAVYTCNEGYQLLGE-INYRECDTDG--WINDIPICEVVKC-LPVTAPENGKIVSSAME 145
                                                                                        submitted to the EMBL Data Library, April 1996 The sequence of C. elegans cosmid T07H6.
                                                                                                                                                                                                                                                                                            T16833 #type complete
hypothetical protein T07H6.5 - Caenorhabditis elegans
formal_name Caenorhabditis elegans
20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
                                                                             T16833
                                                                                                                                                                                 Geisel, C.
                                                                                                                                                                                                                                                       T1683
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10-Sep-1999 #sequence_revi;
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India-1967)
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#map_position 1q22-1q25
CLASSIFICATION #superfam
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                    ene GDB:SELP; GRMP
##CTOSS-Ieferences GDB:120018; OMIM:173610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-830 ##label JOH
##cross-references GB:M25322
##note parts of this sequence, including the amino end of the
mature protein, were confirmed by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 EEMHCSDDGFWSKEKPKCVEISCKS-PDVINGSPISQKIIYKENERFQYKCNMGYEYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 CDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AQWEGPD-LR-CKARACPDPGDIENG----LREGDTFEYPHHVKYSCNPGFLLVGSTS-RQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 GDAVCTESG-WR-PLPSCEEKSCDNPYIPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 SKAKCMEDGQWSAPIPRCLA-SCRVPHIQNG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 VQRICLAEGIWGGNEPRCEEIRCSVLPTLPNGYIEGSETSFGAVAVFRCLETMTHE-GA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##Cross-references EMBL:U53344; NID:g1255886; PID:g1255889; PIDN:AAA96225.1; GSPDB:GN00028; CESP:T07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##experimental_source strain Bristol N2; clone T07H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRE 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 17.4%;
Similarity 32.2%;
68; Conservative
                                                                                                                                                                                                                                                                                                                                                                      #superfamily complement factor H repeat homology;
                                                                                                                                                                                                                                                                                                                    cell adhesion; glycoprotein; phosphohistidine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnston, G.I.; Cook, R.G.; McEver, R.P.
Cell (1989) 56:1033-1044
Cloning of GMP-140, a granule membrane protein of platelets
and endothelium: sequence similarity to proteins involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD62 antigen; granule membrane protein 140 #formal_name Homo sapiens #common_name man 18_OCt-1989 #sequence_revision 30-Sep-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A30359
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P-selectin precursor - human
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#length 560 #molecular-weight 61619 #checksum 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14/1; 75/1; 102/3; 128/1; 186/1; 272/2;
475/1; 527/1
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                                                                                                                                                                                                                                                                                                phosphoprotein; surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                       homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-Aug-1997
#domain complement factor H repeat homology #label FH01\
#domain complement factor H repeat homology #label FH02\
#domain complement factor H repeat homology #label FH03\
#domain complement factor H repeat homology #label FH04\
#domain complement factor H repeat homology #label FH05\
#domain complement factor H repeat homology #label FH05\
#domain complement factor H repeat homology #label FH06\
#domain complement factor H repeat homology #label FH06\
#domain complement factor H repeat homology #label FH06\
#domain complement factor H repeat homology #label FH08\
                                                                                                                                                                                                #domain signal sequence #status predicted #label SIG\
#product P-selectin #status experimental #label MAT\
#domain EGF homology #label EGF\
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Pred. No. 9.92e-58;
42; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
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                                                                                                                                                                                                                                                                                                     FEATURE
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Best Local
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716,723,741
Best Local Similarity 31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54,98,180,212,219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Albrecht, J.C.; Fleckenstein, B.
#journal J. Virol. (1992) 66:3937-3940
#title New member of the multigene family of complement control
#cross-references MUID:92260674
                                                                                                                                                                                                                                                           21-302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                               36,39,46,72,155
                                                                                                                                                      210-264
                                                                                                                                                                     147-205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 TESG-WR-PLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 DNLGQWTAPAPVCQALQCQDLPVPN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 APAPVCKAVQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECQPGYRVRGLDMLRCIDS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 QCLAAQC-PPLKIPERGNMICLHSAKAFQHQSSCSFSCEEGFALVGP-EVVQCTASGVWT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KCQKRPCGHPGDTP-FGTFT-LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 17.0%;
Local Similarity 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFWSKEKPKCVEISCKSPDV-INGS-PISQKI-IYKENERFQYKCNMGYEYSERGDAV-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #length
                                                                                                                                                                                                                                                                                                                                                #superfamily herpesvirus complement control protein;
complement factor H repeat homology
alternative splicing; duplication; extracellular protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #formal_name saimirine herpesvirus 1
30-Jun-1993 #sequence_revision 30-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sccpH protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WMBELE #type complete
secretory complement control protein homolog
saimirine herpesvirus 1 (strain 11)
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                                                                                                                                                                                                                                                                                                                                                                                                                 288/1
                                                                                                                                                                                                                                                                                                                            glycoprotein; transmembrane protein
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#domain transmembrane #status predicted #label TMN\
#domain intracellular #status predicted #label CYT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                    #domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
                                                                                                                               #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                       #domain signal sequence #status predicted #label SIG\
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                                                                                                         predicted
                                                                                         #molecular-weight 33392 #checksum 5963
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Pred. No. 1.49e-55;
                          Score 341; DB 1;
Pred. No. 7.88e-55;
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                                               Length 302;
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1-20
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#journal J. Virol. (1992) 66:3937-3940
#title New member of the multigene family of complement control
#cross-references_MUID:92260674
#cross-references_MUID:92260674
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84-142
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329-345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPRCVEISCKSP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##cross-references EMBL:X60283; NID:g60315; PIDN:CAA42823.1; PID:g60317
[FICATION #superfamily herpesvirus complement control protein; complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 NVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG---WTNDIPICEVVKCLPVTAPENGK 138
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214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC 264
                                                                                              156 GTHTNVK-DF-YTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLP 213
                                                                                                                                                                                               100 NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
                                                   139 IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP 195
                                                                                                                                            84 NVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG---WINDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                           24 YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG
                                                                                                                                                                                                                                                                                         44 YPNGTTLHVTCREGYAKRPVQTVTCVNGNW-TV-P-KKCQKKKCSTPQDLLNGRYTVTG- 99
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30-Jun-1993_#sequence_revision 30-Jun-1993 #text_change
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homolog #status predicted #label SCC\
#domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain transmembrane #status predicted #label TMN\
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Search completed: Thu Jun 8 21:41:41 2000 Job time : 20 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm \*\*\*\*\*\*\*\*\*\*\*\*

Run on: MPsrch\_pp Thu Jun 8 21:41:59 2000; MasPar time 10.76 Seconds 750.375 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-316-163-10 (1-255) from US09316163.pep 2025 1 EDCNELPPERNTEILTGSWS.....EKSCDNPYIPNGDYSPLRIK 265

Sequence:

Scoring table: PAM 150 Gap 11

Searched: 83857 segs, 30454973 residues

Database: Post-processing: Minimum Match 08 Lightng first 45 summaries wiss-prot38

Statistics: Mean 43.808; Variance 61.409; scale 0.713

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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220 220	220	220	219	231	232	238	254	254	257	258	262	270	276	276	276	280	283	284	288	293	
10.8	10.8	10.8	10.8	11.4	11.4	11.7	12.5	12.5	12.7	12.7	12.9	13.3	13.6	13.6	13.6	13.8	13.9	14.0	14.2	14.4	
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#### ALIGNMENTS

RP RA RT	RA RA	RA RA RA	RT	RE RE RE	2000g	DE	RESULT
SEQUENCE OF 19-35. MEDLINE; 83048213. Sim R.B., Discipio R.G.; Purification and structural studies on the complement-system control protein beta 1H (Factor H).";	SEQUENCE OF 1047-1231 FROM N.A.  MEDLINE; 91201892.  MEDLINE; 91201892.  Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss E.H.;  "Cloning of the 1.4-kb mRNA species of human complement factor H  reveals a novel member of the short consensus repeat family related to the carboxy terminal of the classical 150-kDa molecule.";  J. Immunol. 146:3190-3196(1991).	SEQUENCE OF 226-445 FROM N.A., AND PARTIAL SEQUENCE. SEQUENCE OF 226-445 FROM N.A., Tack B.F.; MEDLINE; 86169701. Kristensen T., Wetsel R.A., Tack B.F.; "Structural analysis of human complement protein H: homology with C4b binding protein, beta 2-glycoprotein I, and the Ba fragment of B2."; J. Immunol. 136:3407-3411(1986).	SEQUENCE OF 53-445 FROM N.A.  SEQUENCE OF 53-445 FROM N.A.  MEDLINE; 87054207.  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;  Schwaeble W., Stanley K., Weiss E., Dierich M.P.;  Schwaeble W., Weiss E., Weiss E., Dierich M.P.;  Schwaeble W., Weiss E., Weiss E., Dierich M	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=LIYER; MEDLINE: 88134059. Ripoche J. Day A.J., Harris T.J.R., Sim R.B.; The complete amino acid sequence of human complement factor H."; Biochem. J. 249:593-602(1988).	HFI OR HF OR CFH. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	B8 (	JLT 1 CEAH_HUMAN STANDARD; PRT; 1231 AA.

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EMBL; Y00716; CAA68704.1; -.
EMBL; X04697; CAB41739.1; ALT_FRAME.
EMBL; M65294; AAA35948.1; -.
PIR; S00254; NBHUH.
PIR; S00254; NBHUH.
PIR; S00254; S00254.
PIR; S03013; S03013.
PDB; 1HCC; 15-APR-92.
PDB; 1HFH; 15-JUL-93.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Solution structure of a pair of complement modules by nuclear magnetic resonance.";
J. Mol. Biol. 232:26-284(1993).

-i- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B) NBB COMPLEX (C5 CONVERTASE) CONTINITY COMPLEMENT PATHWAY.

-i- CONVERTASE) IN THE ALITERNATIVE COMPLEMENT PATHWAY.

-i- SIMILARITY: CONVAINS 20 SUSHI (SCR) REPEATS.

-i- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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J. Mol. Biol. 219:717-725(1991).
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ement alternate pathway; plasm
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T -> Q (IN REF. 3).

RP -> IL (IN REF. 2).
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Best Local Similarity 100.0%; Matches 265; Conservative
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 Munoz-Canoves P., Tack B.F., Vik D.P.;
"Analysis of complement factor H mRNA expression: dexamethasone IFN-gamma increase the level of H in L cells.";
Biochemistry 28:9891-9897(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci.
[2]
                                                                                                                                                                              "Demonstration of an unusual allelic variation of mouse factor H by the complete cDNA sequence of the H.2 allotype.";

1. Immunol. 144:358-362(1990)

1. Immunol. 164:358-362(1990)

1. FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION OF CIBES FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF CIBES COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) AND THE (C3B)NB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.
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-Sakai S., Nonaka M., Nonaka M., Harada Y.N., Shreffler D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
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PRECURSOR (PROTEIN BETA-1-H).
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EMBL; M31979; AAA37762.1;
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STRAIN=COPENHAGEN;
                       COMPLETE GENOME
                                                               "The complete DNA sequence of vaccinia Virology 179:247-266(1990).
                                                                                                                                     Goebel
                                                                                                                                                   STRAIN-COPENHAGEN;
MEDLINE; 91021027.
                                                                                                                                                                                                                                  Kotwal G.J., Moss B.; "Analysis of a large cluster of nonessential genes deleted from vaccinia virus terminal transposition mutant."; Virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-WR; MEDLINE; 8
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01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN 35)
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPFCEEKRCSPPYILNGIYTPHRI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDCKGPPPRENSEILSGSWSEQLYPEGTQATYKCRPGYRTLGTIVKVCKNGKWVASNPSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNEKPRCVEILCTPPRVENGDGINVKPVYKENERYHYKCKHGYVPKERGDAVCTGSGWSS
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                                                                                                                           S.J., Johnson G.P., Perkus M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 20-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Vaccinia virus (strain Copenhagen).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1439;
Pred. No. 0.
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W; C5AC02F341B957F7 CRC64;
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                                                                                 virus. ";
                                                                                                                         Davis S.W.,
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                                                                                                                           Winslow
                                                                                                                         J.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X13166; CAA31564.1; -. EMBL; M22812; AAA69605.1; -. EMBL; M35027; AAA47997.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                        REPEA
                                                                                                                                                                                                                                                                                                               REPEAT
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PDB; 1VVD; 03-DEC-97
PDB; 1VVE; 03-DEC-97
                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A31005; WMVZSP.
PDB; 1VVC; 03-DEC-97
154 ISNGR--HNGYE-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WS-DPPTCQIVKCP 207
                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Vaccinia virus complement-control protein prevents antibody-dependent complement-enhanced neutralization and contributes to virulence.",
Proc. Natl. Acad. Sci. U.S.A. 89:628-632(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barlow P.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wiles A.P., Shaw G., Bright J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goebel S.J., Johnson G.P., Perkus M.E., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                     97
                                                                     20 SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT
                                                                                          40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isaacs S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 179:517-563(1990).
                       FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--WTNDIPICEVVKCLPVTA
                                             LDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICESVKCQSPPS
                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 BY NMR OF 146-263.
97446168.
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                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                            Sushi
                                                                                                                                19.1%;
                                                                                                                                                                     28629
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                                                                                                                                                                                                                                                                                                                                                          3D-structure.
                                                                                                                                                                     WW;
                                                                                                                     Score 388; DB 1;
Pred. No. 7.02e-75
37; Mismatches 9
                                                                                                                                                                                                                                                                         COMPLEMENT CONTROL PROTEIN.
4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 3.
                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                  E4322CC9A6EF8997 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis S.W., Winglow J.P.,
                                                                                                                      96;
                                                                                                                                           Length 263
                                                                                                                    Indels 21;
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P04003;
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01-OCT-1993
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4B-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4BPA OR C4BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lintin S.J., Lewin A.R., Reid K.B.M.;
"Derivation of the sequence of the signal peptide in human
C4b-binding protein and interspecies cross-hybridisation of the C4bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.;
"Molecular cloning of the cDNA coding for proline-rich protein (PRP):
identity of PRP as C4b-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic organization protein gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                         Chung L.P., Gagnon J., Reid K.B.M.;
"Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and alignment of the fragments produced by limited proteolysis with chymotrypsin and the peptides produced by cyanogen bromide treatment."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 86301119.
Lintin S.J., Reid K.B.M.;
"Studies on the structure of the human C4b-binding FEBS Lett. 204:77-81(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 9-81 FROM N.A. MEDLINE: 88242821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 174:222-227(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Chung L.P., Bentley D.R., Reid K.B.M.;
"Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 203-288 FROM N.A.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 49-88.
MEDLINE; 85296001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 80-597 FROM N.A.
"Visualization of human C4b-binding protein and its vitamin K-dependent protein S and complement protein Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem.
                                                                                MEDLINE: 832
Dahlback B.,
                                                                                                                              ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244
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                                                                                                                                                                                      Immuno1.
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                                                               83221615.

B., Smith C.A., Mueller-Eberhard H.J.;

and Chabinding protein and
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                                                                                                                                                                                      22:427-435(1985).
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27, Last sequence update)
35, Last annotation update)
IN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
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165:138-144(1989).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS OF 3 POSSIBLE SORTS: A 570 KD COMPLEX OF TALPHA CHAINS AND 1 BETA CHAIN, A 530 KD HOMOHEDTAMER OF ALPHA CHAINS OR A 500 KD COMPLEX OF ALPHA CHAINS OR A 500 KD COMPLEX OF ALPHA CHAINS OR A 500 KD COMPLEX OF ALPHA CHAIN SON AND 1 BETA CHAIN. THE CENTRAL BODY OF THE ALPHA CHAIN HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE BINDING STAPE FOR ALPHA CHAIN SON AND THE SUPPORTS TENTACLES, EACH WITH THE BINDING
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TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.
TISSUE SPECIFICATY: CHYLOMICRONS IN THE PLASMA.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
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M62476; AAA36506.1;
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Kristensen T.;
"Structure of the human beta-2-glycoprotein I gene.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q01339;
Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-APR-1999 (Rel. 35, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) (BZGPI).
                                                                                     SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE LIVER;
                                                                                                                                                     "Characterization, expression and evolution of mouse beta glycoprotein I (apolipoprotein H)."; glycoprotein Biochem. Biophys. Res. Commun. 200:1521-1528(1994).
                                                                                                                                                                                                                                                                 Sellar G.C.,
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"Molecular cloning of mouse beta
gene to chromosome 11.";
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10056; BAA00945.1; --
EMBL; S70439; AAB30789.1; --
EMBL; Y11356; CAA72190.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A43286; NBMS
                                                                                                                                                                       81
                                                                                                                                                                                                                 23 TYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
                                                                                                                                                                                                                                            40 SYDDGEQIVYSCKPGYVSRGGMRRETCPLTGMW-PINTLR-CVDRVCPFAGILENGIVRY
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- TISSUE SPECIFICITY: PLASMA.
- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                              Local
                                                NG--S-PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSCDNPYI
                                                                         NGYVNYPAKPVLLYKDKATFG--CHETYKLDGPEEAECTKTGTWSFLPTCRE-SCKLPVK 269
                                                                                                      VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK-SPDVI 198
                                                                                                                                KDYRPSAGNNSLYQDTVVFKCLPHFAMIGNDTVMCTEQGNWTRL-PECLEVKCPFPPRPE
                                                                                                                                                           TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                       TS---FEYPKNISFACNPGF-FLNGTSSSKCTEEGKWSPDIPACARITCPPPPVPKFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:88058; APOH.
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                                                                                                                                                                                                                                                                                           h 18.3%;
Similarity 29.4%;
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                                                                                                                                                                                                                                                                                Conservative
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183
193
252
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                                                                                                                                                                                                                                                                                          Score 371; DB 1;
Pred. No. 3.37e-70;
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4 X SUSHI (SCR) REPEATS
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                                                                                                                                                                                                                                                                                                                               C83F8A6EBD51C940 CRC64;
                                                                                                                                                                                                                                                                           Mismatches 110; Indels 19;
                                                                                                                                                                                                                                                                                                                                                 R (IN REF.
                                                                                                                                                                                                                                                                                                    Length 345;
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                    80
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C4BP_RAT
Q63514;
Q1-NOV-1997
01-NOV-1997
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structural and functional relati mouse, and rat proteins.";
J. Immunol. 158:1315-1323(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Rodentia;
                                    DISULFID
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                                                                             DISULFID DISULFID
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: C48P CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. I ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN AND WITH SERUM AMYLOID P COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathway; Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN ALPHA CHAIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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35, Last sequence update)
36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4b binding protein alpha-
relationships among human,
SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

SUSHI 5.

SUSHI 6.

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BY SIMILARITY.

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BY SIMILARITY
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8 X SUSHI (SCR) REPEATS.
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thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558
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ae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
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bovine, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
          (POTENTIAL)
                            (POTENTIAL)
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CARBOHYD
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                endothelium: sequence similarity to proteins involved
adhesion and inflammation.";
Cell 56:1033-1044(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SELP OR GMRP.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P16109;
   Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,
Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,
Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
The p-selectin gene is highly polymorphic: reduced frequency of the
Pro715 allele carriers in patients with myocardial infarction.";
Hum. Mol. Genet. 7:1277-1284(1998).
-!- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
-!- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THE
TO CARROHYDRATES ON MEDITAPELIS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnston G.I., Cook R.G., McEver R.P.; "Cloning of GMP-140, a granule membrane protein of platelets and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                       Bajorath J., Stenkamp R., Aruffo A.; "Knowledge-based model building of proteins: concepts and examples.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEM3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 INSGFKHTYKYKDSVRFVCQKGFVLRGSGVIHCEADGSWSPVPVCELNSCTDIPDIPNA 272
                                                                                                                                                                                                                                                                                                                     Furie B.;
                                                                                                                                                                                                                                                                                                                                    Freedman S.J.,
                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 160-199
                                                                                                                           VARIANTS ASN-331; ASP-603; VAL-640 AND PRO-756
                                                                                                                                                                           Protein
                                                                                                                                                                                                                          MEDLINE; 94093388.
                                                                                                                                                                                                                                     3D-STRUCTURE MODELING OF 42-161
                                                                                                                                                                                                                                                                        Biochemistry 35:13733-13744(1996).
                                                                                                                                                                                                                                                                                                   "Structure and function
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                                                                                                                                                                                                                                                                                                                                    Sanford D.G., Bachovchin W.W., Furie B.C., Baleja J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     in cell
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EMBL; M60223; p
EMBL; M60223; p
EMBL; M60224; p
EMBL; M60224; p
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EMBL; M60227; p
EMBL; M60227; p
EMBL; M60229; p
EMBL; M60229; p
                                                                                                                                                                                                                                                                                                                                             PFAM; PF00008; EGF; 1.
PFAM; PF00059; lectin_c; 1.
PFAM; PF00084; sushi; 9.
Cell adhesion; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00343; SELECTIN.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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                                                                                                                                                                                                                                                                                                                                     Selectin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE CELL SURFACE.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 9 SUSHI (SCR) REPEATS.

DATABASE: NAME-PROW; NOTE-CD guide CD62P entry;

www-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A30359; A30359.
1FSB; 01-APR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1KJD; 03-APR-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M60233; AAA35910
                  42
772
796
159
199
199
261
323
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447
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1641
163
168
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                                                                                                                                                                                                                                                                                                                                    Sushi; Repeat;
                                                      SUSHI 1.
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EGF-LIKE.
9 X SUSHI
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                                                                                                                                                                                                                                                                                                        P-SELECTIN
                                                                                                                                                                                                                  SUSHI (SCR) REPEATS
                                                                                                                                                                                                                                                                                                                                 Polymorphism; 3D-structure
                                                                                                                                                                                                                                               LECTIN (SHORT FORM)
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01-APR-1993
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                                                                                                                                                                                                                                                           314 APAPVCKAVQCQHLEAPSEGTM-DC-VHPLTAFAYGSSCKFECOPGYRVRGLDMLRCIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                  GHWSAPLPTCEAISCEPLESPVHGSMDCSPSLRAFQYDTNCSFRCAEGFMLRG-ADIVRC
                                                                                                                   TESG-WR-PLPSCEEKSCDNPYIPN
                                                                                                                                                                       GFWSKEKPKCVEISCKSPDV-INGS-PISQKI-IYKENERFQYKCNMGYEYSERGDAV-C
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Similarity 26.0%;
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Pred. No. 8.01e-63;
56; Mismatches 122; Indels 18;
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/FTId=VAR_004195.
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Best Local
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Albrecht J.-C., Fleckenstein B.;
"New member of the multigene family of complement control proteins herpesvirus salmiri.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X64346; CAA45626.1; -. EMBL; X64346; CAA45627.1; -. EMBL; X60283; CAA42823.1; -. EMBL; X60283; CAA42822.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                     CHAIN
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PIR; S24567; S24567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Primary structure of the herpesvirus saimiri genome.";
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                           Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                  HSSP; P10998; 1VVC.
PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                  PIR; B42534; WMBE2E.
                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                               DISULFID
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                                                           VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VITOL. 66:3937-3940(1992).

ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND A SECRETED FORM ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).

SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
Similarity 74; Conser
                                                                                                                                                                                                                                                                                                                                        Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92333688
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83
83
146
209
328
 Conservative
                                                Ą,
                                                                                                                                                                                                                                                                                                                                         Sushi;
                                                              360
            16.8%;
                                                40006 MW;

    Transmembrane; Alternative splicing;

Score 341; DB 1; Leux
Pred. No. 5.23e-62;
                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                     POTENTIAL.
COMPLEMENT CONTROL PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                        SUSHI 3
                                                           RICNGNCTTSMPTQ -> AECACPGSNYPISS
SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
                                                                                                                       POTENTIAL.
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                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the serum complement system.";
Biochemistry 26:4668-4674(1987).
-i- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO MITH SERUM ANYLOID P COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P08607;
01-AUG-1988 (Rel. 08,
01-FEB-1994 (Rel. 28,
01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C4BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C4B-BINDING PROTEIN PRECURSOR (C4BP).
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cDNA structure of murine C4b-binding protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 88024997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4BPA OR C4BP.
                                                           REPEAT
REPEAT
REPEAT
                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
-!- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 DVING-SPISQKIIYKENERFQYKCNMGYE-YSERGDAVCTESGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 QVANAYVEVRKSATSMQYLHINVKCYKGFMLYGETPNT-CNHGVWSPAIPEC
                                                                                                                                                    CHAIN
                                                                                                                                                                  Complement
                                                                                                                                                                                               PFAM;
                                                                                                                                                                                                                                           PIR; A27117
                                                                                                                                                                                                                                                         EMBL; M17122; AAA37312.1; ALT_INIT.
                                               REPEAT
                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMOHEPTAMER; NOT COVALENTLY LINKED. MOUSE LACKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVFEYGVKAVYTCNEGYOLLGEINYREC--DIDG---WINDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLY-YGSVITYTCNSGYSLIGSTT-SACLLKRGGRVDWTPRPPICDIKKCKP--PPQIAN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETA CHAIN OF C4BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVSSAMEPDREYHFGQAVRFVCNSGYKIE--GDEEMHCSDDGFW-SKEKPKCVEISCKSP
                                                                                                                                                                                                              MGI:88229; C4BP.
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                                                                                                                                                                                                PF00084; sushi;
                                                                                                                                                                                                                           P10998; 1VVC
                                                                                                                                                                                pathway;
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                                                                                                                                                                                  Glycoprotein; Repeat; Sushi; Signal.
                                                                                                                       6 X SUSHI (SCR) REPEATS.
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Best Local
                                                                                                                                                                                                                                                 "Cloning, sequence comparison and in vivo expression encoding rat P-selectin.";
Gene 145:251-255(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEM3_RAT STANDARD; PRT; 768 AA.

P98106;

998106;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)

(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammali
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 GNGNWSSLPTCEF-DCDLPPAIVNGYYTSM 317
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FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALVI-LEWIS X.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,
LUNG, BRAIN, LIVER, HEART, KIDNEY, THYMUS, SMALL INTESTINE.
INDUCTION: ACUTE INFLAMATION (PROBABLY).
SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 PPPAIPNALPASDVNRTDFESHTTLKYECLPGYGRGISRMMYYCKPSGEW-EIS-VS-CA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPECVIVKCGPPPDISNGK-HSGT-E-DF-YPYNHGISYTCDPGFRLVGSPFIGCTVVNK
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Pred. No. 5.23e-62;
57; Mismatches 109
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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-!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; RAT P-LECTIN LACKS THE HUMAN SUSHI-2 EQUIVALENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adhesion; Transmembrane; Glycoprotein;
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ENDOCYTOSIS SIGNAL (PROBA CACC64; 26FD7E8A5F3F1316 CRC64;
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C-TYPE LECTIN (SHORT FORM).
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                                  (PROBABLE).
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Query Match

16.8%;

Score 341;

DB 1;

Length 768

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BOS taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metaztiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q28065;
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Immunol. 153:4190-4199(1994).

ITIMUNOL. 153:4190-4199(1994).

IT BINDS AS A COFACTOR TO COBPLEMENT
ACTIVATION. IT BINDS AS A COFACTOR TO COBPLEMENT CABLINATOR
(COBPINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT CABL IT
ALSO ACCELERATES THE DEGRADATION OF THE CABCZA COMPLEX (C3
CONVERTACE) BY DISSOCIATING THE COMPLEMENT FRAGMENT CZA. ALPHA
CHAIN BINDS CAB. IT INTERACTS ALSO MITH SERUM AMYLOLU P COMPONENT.

ISUBUNIT: DISULFIDE-LINKED COMPLEX OF CABP ALPHA AND BETA CHAINS
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4BPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillarp A., Thern A., Dahlbaech B.;
"Bovine C4b binding protein. Molecular cloning of the alpha and beta-chains provides structural background for lack of complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 FECQPGYRMRGSDILHCTDSGQW-S-EPLPTCEAIAC-EPLESPLHGSMDCFPSTGAFGY 346
                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
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P10998; 1VVC.
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BY SIMILARITY
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SUSHI 4.
SUSHI 5.
SUSHI 6.
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LEM3_MOUSE STANUARD.,

Q01102;

Q01102;

Q1-APR-1993 (Rel. 25, Created)

O1-APR-1993 (Rel. 25, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)

CCD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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                      Weller A., Isenmann S., Vestweber D.;
"Cloning of the mouse endothelial selectins. Expression of both and p-selectin is inducible by tumor necrosis factor alpha.";
J. Biol. Chem. 267:15176-15183(1992).
                                                                    SEQUENCE FROM N.A.
MEDLINE; 92340571.
                                                                                                                                                                                                                                                                                                                                                                    135
                                                                                                                                                                                                                                                                                                                                                                                                                                       123 VIVKT-D-YSFGSEIEFSCSEGYVLIGSANSYCQLQDKGVVWSDPLPQCIIAKCEPPPTI 180
SEQUENCE FROM N.A
                                                                                                       Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDQTYPEGTQAIYKCRPGYR-SLGNVIMVCR-KGEWVALNPLRKCQKRPCGHPGDTPFGT 77
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27.5%;
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                                                                                                       Chordata; Craniata; Vertebrata; sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 338; DB 1;
Pred. No. 3.41e-61
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MGD: MGI998280; SELECTIN.
PROSITE: PRO0343; SELECTIN.
PROSITE: PS00322; EGF_1; 1.
PROSITE: PS01186; EGF_2; 1.
PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                             REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                           DOMAIN
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-!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
THE HUMAN SUSHI-2 EQUIVALENT.
                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanders W.E. Jr., Wilson R.W., Ballantyne C.M., Beaudet A.L.; "Molecular cloning and analysis of in vivo expression of murine p-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHERIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                      PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P16109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80:795-800(1992)
                                                                                                                                                                                                                                                                                                                                                               Signal; Sushi; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92345617.
                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                  lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                EGF;
  SUSHI
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IHSUS
IHSUS
IHSUS
                                                                                                                                                               SUSHI
                                                                                                                                                                                        SUSHI
                                                                                                                                                                                                                                                                                    C'TYPE LECTIN
                                                                                                                                                                                                                                                     SUSHI
                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
Y SIMILARITY
                                                                                                                                                                                                                                                               X SUSHI
                                                                                                                                                                                                                                                                                    (POTENTIAL).
IN (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                    EGF-like domain; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and the EMBL outstation
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Best Local
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                                                            beta
   MEDLINE; 90226:
Li Q., Blacher
              SEQUENCE OF 20-41. MEDLINE; 90226328.
                                                                                 Kato
                                                                                                                                  "Complete primary structure of bovine localization of the disulfide bridges. Biochemistry 31:3611-3617(1992).
                                                                                                                                                                                                                                               TISSUE=LIVER;
Gao B., Virmani M., Romm E.,
Appella E., Kunos G., Takacs
                                                                                                                                                                                                                                                                                                                                                    APOH_BOVIN STANDARD; PRT; 345 AA. P17690; Q28052; 01-AUG-1990 (Rel. 15, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H).
                                               Biochemistry
                                                                                          MEDLINE;
                                                                                                                                                                               Bendixen E., Halkier T., Magnusson
                                                                                                                                                                                            TISSUE-LIVER;
MEDLINE; 92232647.
                                                                                                                                                                                                              SEQUENCE OF 4-345 FROM N.A., PARTIAL SEQUENCE,
                                                                                                                                                                                                                                   Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                               SEQUENCE OF 20-345,
                                                                                                                                                                        Kristensen
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID DISULFID
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                                                                                                      ISSUE=PLASMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 FSFNSQCTFSCAEGYELDGPGEL-QCLASGIWTNNPPKCDAVQCQSLEAPPHGTM-AC-M 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVPSTGTFGYNSSCTFLCAEGFVLKGNDAIQCADSGQWTAPAPFCEALQC 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAM 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV-INGS-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPIAAFAYDSSCKFECQPGYRARGSNTLHCTGSGQWSEPLPTCEAIACEPPEIPIHGSMD
                                                      E; 92089075.

Brjyoji K.-I.;

acid sequence and location of the acid sequence in I: the presence of fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.7%;
Similarity 30.0%;
51; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           756
724
768
                                            30:11687-11694(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505
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83098
Esch F., Congote L.F.;
                                                                                                          CARBOHYDRATE-BINDING SITES, AND DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 339;
Pred. No. 1.
35; Mismatc
                                                                                                                                                                                                                                                           Lazar-Wesley E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENDOCYTOSIS SIGNAL (PROBABLE).
A -> E (IN REF. 2).
E5173074D2F66E68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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                                                                                                                                                                               s.,
                                                                                                                                                beta 2-glycoprotein
.";
                                                       five
                                                                                                                                                                             Sottrup-Jensen L.,
                                                                                                                                                                                                                                                                                                              Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
..83e-61;
                                                                  disulfide
                                                      Sushi domains.
                                                                                                                                                                                                                                                           Sakaguchi
                                                                                                                                                                                                             AND DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 768;
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                                                              bonds in
                                                                bovine
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                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its up non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erythroid cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heparin-binding;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S23597;
PIR; S09032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation from fetal bovine serum of an apolipoprotein-H-like protein which inhibits thymidine incorporation in fetal calf
                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                     DISULFID
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                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                  SEQUENCE
                                                                                                                                                              CONFLICT
                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                               CARBOHYD
153 LSVYKPLAGNNSFYGSKAV-FKCLPHHAMFGNDTVTCTEHGNWT-QLPECREVRCPFPSR 210
                   80 LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGK 138
                                      97
                                                        22
                                                                          39 RTYEPGEQIVFSCQPGYVSRGGIRRFTCPLTGLW-PINTL-KCMPRVCPFAGILENGTVR 96
                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chem. J. 267:261-264(1990).

FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HERARIN. PHOSPHOLIPIDS, AND CEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L07303; AAA30382.1;
x60065; CAA42669.1;
                                     YT---TFEYPNTISFSCHTGFYLKGASSAK-CTEEGKWSPDLPVCAPITCPPPPIPKFAS 152
                                                        QTYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSUE SPECIFICITY: PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
                                                                                                       Similarity
                                                                                                                                                                                S09032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NBBO
                                                                                            Conservative
                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Plasma; Repeat; Sushi; Signal.
                                                                                                      16.5%;
29.1%;
                                                                                                                                   38252 MW;
                                                                                              44;
                                                                                                      Score 334; DB 1;
Pred. No. 4.13e-60;
                                                                                                                                                                                                                                                                                                                                                                                            SUSHI 2.
SUSHI 3.
SUSHI 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 4 X SUSHI (SCR) REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                    MODIFIED-SUSHI
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                                                                                              Mismatches
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N
                                                                                                                                                     REF.
                                                                                               104;
                                                                                                                Length 345;
                                                                                                                                    CRC64;
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01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST
          Cervoni F., Fenichel P., Akhoundi C., Hsi
"Characterization of a cDNA clone coding
cofactor protein (MCP, CD46).";
                                                                                                                                                                                                                                                                                                                                                                                                  Purcell D.F., Russell S.M.,
McKenzie I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cofactor protein (MCP). Evidence for inclusion in the multigene family of complement-regulatory professes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lublin D.M., Liszewski M.K., Post T.W., Arce M.A., le Beau M.M., Rebentisch M.B., Lemons R.S., Seya T., Atkinson J.P.; "Molecular cloning and chromosomal localization of human membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 88286080.
Lublin D.M., Lisze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 I-VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK--S- 194
                                                                                                                                                                                                                                                         "Characterization of the promoter region of the membrane cofactor protein (CD46) gene of the human complement system and comparison to a membrane cofactor protein-like genetic element.";
                                                                                                                                                                                                                                                                                                                                                                        "Alternatively spliced RNAs encode several isoforms of CD46 (MCP), regulator of complement activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                            +
                                                                                                                                                                             Russell S.M., Sparrow R.L., McKenzie I.F.C., Purcell D.F.J.; "Tissue-specific and allelic expression of the complement regulator
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 PDNGFVNHPANPVLYYKDTATFG--CHETYSLDGPEEVECSKFGNWSAQPSCKA-SC
                                                                                                                                                                     CD46
                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                Kumar V
                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-34 FROM N.A.
                                                                                                                                                                                                                     ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                              [mmunogenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exp. Med
                                                                                                                                                                                                                                             Immunol. 151:4137-4146(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDV-INGSPISOKITYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSC
  GAMMA ISOFORM (TRANSCRIPTS A AND B) IS PREFERENTIALLY EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reprod. Dev. 34:107-113(1993).
                                                                                                                                                                                                                                                                                                           Hourcade
                                                                                                                                                                                                                                                                                                                                                                                                                           91267562
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                                                                                                                                                                                                                                                                                                                          94014356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement-regulatory proteins.";
                                                                                                                                                                                                        92289809.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168:181-194(1988).
                                                                                                                                                                                                                                                                                                                                                               33:335-344(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                           D., Post T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 35-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Akhoundi C.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Deacon N.J., Brown M.A., Hooker D.J.,
                                                                                                                                                                                                                                                                                                              Greenlund A.C., Atkinson J.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hsi B.L.,
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                              Matches
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EMBL; S51940; AAR24802.1; ...
EMBL; M58050; AAA62833.1; ...
EMBL; A18585; CAA01400.1; ...
EMBL; S65879; AAD13968.1; ...
PIR; S01896; S01896
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VARSPLIC
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DOMAIN
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long are its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                      VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement
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33 DACEE-PPTFEAMELIGK-PKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVS 90
                             Local Similarity
les 81; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EBV-B CELLS AND LEUKEMIC CELLS. THE 66 KD ALPHA ISOFORM AND THE 56 KD BETA ISOFORM FOUND IN ALL TISSUES EXCEPT SPERM CORRESPOND TO THE TRANSCRIPTS C AND D, AND THE TRANSCRIPTS E AND F RESPECTIVELY.

THE EXON 9 IS SPECIFICALLY DELETED IN SOME PLACEMYAE. THE EPSILON ISOFORM CORRESPONDS TO THE TRANSCRIPTS I AND J. SPERMATOZOA DELTA ISOFORM (TRANSCRIPT N) DELETE BOTH EXONS 12 AND 13. ALL TISSUES DIFFERENTIALLY SPLICE EXON 13.

TISSUE SPECIFICITY: EXPRESSED BY ALMOST ALL CELLS EXCEPT ERYTHROCYTES AND SOME BONE MARROW CELLS.
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DATABASE: NAME-PROW; NOTE-CD guide CD46 entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd46.htm".
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                                                                          377 AA;
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                            Conservative
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31.0%;
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                                                                         MW;
                          Score 335; DB 1;
Pred. No. 2.22e-60;
54; Mismatches 99
                                                                                                      RG (IN ISOFORM B/D/F/H/J/L).
MISSING (IN ISOFORM M AND ISOFORM N).
MISSING (IN ISOFORM N).
                                                                                                                                       MISSING (IN A SECOND FORM).

MISSING (IN ISOFORM M).

YLORRKKKG -> DIFKGGRRKGKOMVELNMPLTRLNOPLO
OSREAE (IN ISOFORM M).

TYLDETHREVKETSL -> KADGGAEYATYQTKSTTPAEQ
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SUSHI 1.
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MEDIINE; 92135065.

Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K., Yasuda T., Koike T.;

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                                                                                                                                                                                                                       Day J.R., O'Hara P.J., Grant F.J., Lofton-Day C.E., Berkaw M.N., Werner P., Arnaud P.; "Molecular cloning and sequence analysis of the cDNA encoding huapolipoprotein H (beta 2-glycoprotein I).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P02749;
21-JUL-1986 (Rel. 01, Created)
01-UN-1994 (Rel. 29, Last sequence update)
15-FEBS-200 (Rel. 39, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) (B2GPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence and expression of the human apollopprotein H (beta 2-glycoprotein I).";
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 92273779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
MEDLINE; 92084151.
MeDdi H., Nunn M., Steel D.M., Whitehead A.S., Perez M., Walker L.,
Peeples M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steinkasserer A., Estalle "Complete nucleotide and glycoprotein I.";
                                                                                                                                                       SEQUENCE FROM N.A.
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"Molecular cloning and mammalian expression of human beta
2-glycoprotein I cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kristensen T.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; (
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                                                                                                                                                                                                         Lab. Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 20-345, CARBOHYDRATE-BINDING SITES, AND DISULFIDE BONDS
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Hum. Genet. 100:57-62(1997).
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Campbell I.D., Sim
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MEDLINE; 93050249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid polymorphism.";
Hum. Genet. 91:401-402(1993).
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                                                                                                                                                                                                                                                             Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.; "Identification of structural mutations in the fifth domain of polipoprotein H (beta-2-glycoprotein I) which affect phospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT ASN-107
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                                                                                                                                                                                                                  Hum. Mol. Genet.
-!- FUNCTION: BIN
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or send an email to license@isb-sib.ch).
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                                                                                                                FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
TISSUE SPECIFICITY: PLARMA.
SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
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                                                                                                           Local
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B43286; B43286
                                                                 YPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTLT 81
                                                                                 YEPGEEITYSCKPGYVSRGGMRKFICPLTGLW-PINTL-KCTPRVCPFAGILENGAVRYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y11494;
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                                GGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKI-
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Y11497; CAA72279.1;
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               VYKPSAGNNSLYR-DTAV-FECLPQHAMFGNDTITCTTHGNWTKL-PECREVKCPFPSRP 211
                                               ---TFEYPNTISESCNTGFYLNGADSAK-CTEEGKWSPELPVCAPIICPPPSIPTFATLR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X53595;
                                                                                                  Similarity 72; Conse.
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                                                                                                                                    345 AA;
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CAA37664.1;
CAA40977.1;
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CAA72279.1;
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Pred. No. 7.71e-60;
43; Mismatches 102
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S -> C (IN REF.
C -> N (IN REF.
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V -> L (IN 23% OF THE POPULATION).
/FTId=VAR_000673.
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                                                                                                                   Length 345;
                                                                                                     Indels 22;
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                                                                                     98
                                                                                                      18;
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Дb Qγ 

Search completed: Thu Jun 8 21:42:12 2000 Job time: 13 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jun 8 21:42:31 2000; MasPar time 26.07 Seconds 704.848 Million cell updates/sec

Tabular output not generated.

Run on:

Description: Perfect Score: >US-09-316-163-10 (1-265) from US09316163.pep 2029

Sequence: 1 EDCNELPPRRNTEILTGSWS.....EKSCDNPYIPNGDYSPLRIK, 265

Scoring table: PAM 150 Gap 11

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics: Nean-43.031; Variance 62.408; scale 0.690

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4.56e-58	. •		0 1.53e-62 2 81e-62		1.34e-63	3.960-64		_		# 4.65e-/5	3.000-81	1.61e-81			<u></u>		Pred. No.

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2.79e-57 1.70e-56 1.70e-56 1.70e-56 5.68e-56 5.68e-55 6.30e-55 6.30e-54 2.11e-54 2.11e-54 2.31e-53 3.11e-53 3.11e-53 3.24e-51 3.24e-51 3.24e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49 5.88e-49	2.79e-57

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.0%; Score 2029; DB 4; Length 449;	POTENTIAL. POTENTIAL. 933 MW; 61231E1B CRC32;	·	1; ;	⊒	1;	gia, Hospital Trias I Pujol, Spain.	Α.		; the FMHI/GenBank/DDBJ databases:	A.		136:3407-3411(1986).	coprotein I, and the Ba fragment of	TACK B.F.;		M N.A.			nce of human complement factor	HARRIS T.J.R., SIM R.B.;			arrhini; Hominidae; Homo.	н			OR LUCK	<ol> <li>Last sequence update</li> </ol>	ted)	PRT; 449 AA.	
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      Q91275
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
02P MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
Bos taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOAMES C.J., DAY A.J., SIM R.B.; "Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b."; Biochem. J. 315:523-531(1996).
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Q28085;
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                                                                                         187 RP 188
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                             200 GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDY 259
                                                                                                                                     127 GOAVLPKATYKONERVOYRCAAGFEYGORGDTVCTKSGWTPAPTCIEITCDPPRIPNGVY 186
                                                                                                                                                                      140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
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                                                                                                                                                                                                 67 FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPPVILN 126
                                                                                                                                                                                                                                80 LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKI 139
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                                                                                                                                                                                                                                                                                                              Match 46.98;
Local Similarity 64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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; 75683 MW; FAF0D174 CRC32;
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Pred. No. 4.00e-230;
29; Mismatches 36; Indels
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9WRUZ;
Q1-NOV-1999 (TrEMBLrel. 12, C;
Q1-NOV-1999 (TrEMBLrel. 12, L;
Q1-NOV-1999 (TrEMBLrel. 12, L;
COMPLEMENT BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.9%; Score 587; DB 13; Length 1053; Best Local Similarity 37.1%; Pred. No. 7.83e-127; Matches 91; Conservative 41; Mismatches 101; Indels 12
                                                                                                                                                              Balliana Bal
                                                                                                                                                                                                                                                                                           MEDLINE; 99174001.
SEARLES R.P., BERGQUAM E.P., AXTHELM M.K., WONG S.W.;
"Sequence and genomic analysis of a Rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated herpesvirus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta rhadinovirus 17577.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9WRU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem J. 301:391-397(1994).

EMBL; L21703; AAA,9256.1; -.

HSSP; P08603; HEH.

PFAM; PF00084; Sushi; 16.

SEQUENCE 1053 AA; 117597 MW; ODF68EDB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91275;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TREMBLREL. 12, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
21.5%;
Local Similarity 30.9%;
es 72; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 GDYSP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 SSAMEPDREYHFGQAVREVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neblifer).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paralabrax nebulifer (barred sand bass).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Repopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Perciformes; Percoidei; Serranidae; Paralabrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 TRYEP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 GSPISQKIIYKENERFQYKCNMGYEYSERGDA-V--CTESGWRPLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 IGG--PE-EATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of a cDNA representing a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 EASYPGGRQVRVGCNVGY-S-GFFKLVCVEGKWETRGA--KCQPRSCGHPGDAQFADFHL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNVPGAIREYKENDVLHYECDRAFKHIDRPSTCIKQGIKAEWSPTPLCESIKCRLTIMDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory plasma protein from barred sand bass (Parablax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAIDOH T., ZIPFEL P.F., GIGLI I.;
         Score 436; DB 14;
Pred. No. 2.63e-85;
50; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                 60FB82D6 CRC32;
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                                                                                 Length 645;
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040912;
01-JAN-1998
01-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U93872; AAB62602.1; -. HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEIPEL F., ALBRECHT J.C., FLECKENSTEIN B.;
"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?";
J. Virol. 71:4187-4192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 97296220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455
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                                                                                                     01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                        Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                      P88903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
SEQUENCE FROM N.A. MEDLINE; 97121480.
                                         Gammaherpesvirinae; Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                           110
                                                                                                                                                                                                                                  204
                                                                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 RCRSGYTTYARNITATCLQGGTW-S-EPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG 109
                                                                                                                                                                                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 20.8%;
Local Similarity 31.9%;
es 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESGW-RPLPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITNGKY--HPVK-DF-YQYLDTVTFSCNRDFSLVGDEMTTCISNT-WNKPFPRCEQITCS 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTGG-NVFEYGVKAVYTCNEGYQLLGE-IN-Y--REC-DTDGWINDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTSGEDAFKYGTNITYKCNEGYQLLGSMVRICMLKDDLKTVDWEPKAPICDIEKCKPPPQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKYSVGASVELICRÞGFTKMOSTVSVECLSNGTWTAÞNA--KCHRKKCÞTÞQELLNGEYI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APNIAHGKLLTGSSSVYKYGQSVTIGCETGFTLIGSEISTCKDSSWDPPLPTC 562
                                                                                                                                                                                                                                                                                                EPDREYH-FGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI
                                                                                                                                                                                                                                                                                                                              KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI 223
                                                                                                                                                                                                                                                                                                                                                             VKAVYTCNEGYQLLG-E-INYRECDTDG---WTNDIPICEVVKCLPVTAPENGKIVSSAM 144
                                                                                                                                                                                                                                                                                                                                                                                          ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-H-R-P---KIENGDF 163
                                                                                                                                                                                                                                SQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESGW-RPLPSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                QGFSLTYKHKQSVTFACNDGFVLRGSPTITCNVTEWDPPLPKCVLEDIDDPNNSN 278
                                                                                                                                                                                                                                                                                                                                                                                                                           KCRPGYRSLG-NVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 422; DB 14;
Pred. No. 1.61e-81;
46; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558089B4 CRC32;
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                                                                                                                                                                           550 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 550;
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EMBL; U75698; AAC57082.1; ...
HSSP; P10998; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOORE P.S., BASHOFF C., WEISS R.A., CHANG Y.;
"Molecular mimicry of human cytokine and cytokine response pathway
genes by KSHV.";
genes by KSHV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RUSSO J.J., BOHENZKY R.A., CHIEN M.C., CHEN J., YAN M., MADDALENA D., PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00084; sushi; 4
SEQUENCE 550 AA; 6068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY 1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
41KBP FRAGMENT FROM LEFT END OF GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D17L OR C17L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P87616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P87616
                                                                                                                                                                                                                                        MEDLINE: 98229462.
SHCHELKUNOV S.N., SAFRONOV P.F., TOTMENIN A.V., PETROV N.A., SHCHELKUNOV S.N., GUTOROV V.V., KOTWAL G.J.;
RYAZANKINA O.I., GUTOROV V.V., KOTWAL G.J.;
"The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cowpox virus (CPV).
                                                                                                                                                                                                     Lerminal region of a cowpox virus strain reveals unique sequences a cluster of intact ORFs for immunomodulatory and host range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 97068532.
SAFRONOV P.F., PETROV N.A., RIAZANKINA O.I., TOTMENIN A.V., SHCHELKUNOV S.N., SANDAKHCHIEV L.S.;
"Genes of a circle of hosts for the cowpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-GRI-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-GRI-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dokl. Akad. Nauk 349:829-833(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI 223
                                                          EMBL; X94355; CAA64102.1; -.
EMBL; Y11842; CAA72567.1; -.
HSSP; P10998; IVVC.
                                                                                                                                                       proteins.";
Virology 243:432-460(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 SQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESGW-RPLPSCEEKSCDNPYIPN 256
   PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 KCRPGYRSLG-NVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 RCRSGYTTYARNITATCLQGGTW-S-EPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKAVYTCNEGYQLLG-E-INYRECDTDG---WINDIPICEVVKCLPVTAPENGKIVSSAM 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-H-R-P---KIKNGDF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPDREYH-FGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI
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Similarity 31.9%;
75; Conservat'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97094384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEA2CAEC CRC32;
                76531F63 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAY A.J., RIPOCHE J., LYONS A., MCINTOSH B., HARRIS T.J., SIM R
"Sequence analysis of a cDNA clone encoding the C-terminal end numan complement factor H.";
Biosci. Rep. 7:201-207(1987).
EMBL; M17517; AAA52016.1; -.
HSSP; P08603; 1HFH.
EFAM; PF00084; sushi; 11.
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Q14006;
239 RPLPSCEEKS--CDNPY-IPNGDYSPLRI 264
                                                       523 TEPPQCKDSTGKCGPPPPIDNGDITSFPL 551
                                                                                                                                     182
                                                                                                                                                                                             465
                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                             409
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Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENT H FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 CSQ-PPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKW-S-SP-PQ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CNELPPRRNTEILTGSWSDQ-TYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 27.5%; ss 74; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--W 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 QCIKRRCPSPRDIDNGQLDI-GG-V-DFGSSITYSCNSGYHLIGESKSYCELGSTGSMYW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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                                                                                                            KEKPKCVEISC-KSPDVINGSPIS-QKIIYKENERFQYKCNMGYE-YSERGDAVCTESGW
                                                                                                                                                                 -GRPTCRDTSCVNPPTVQNAYIVSRQMSKYPSGERVRYQCRSPYEMFGD-EEVMCLNGNW 522
                                                                                                                                                                                                                         ICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWS 181
                                                                                                                                                                                                                                                                                 SCIKTDCLSLPSFENA-IPMGEKK-D-VYKAGEQVTYTCATYYKMDGASNVTCINSR-WT 464
                                                                                                                                                                                                                                                                                                                                               CQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                  CEGLPCKSPPEISHGVVAHMSDS-YQYGEEVTYKCFEGFGIDGPAIAK-CLGEKWSHP-P 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGFWSKEKPKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG-WRP-LPSC 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657 AA; 74247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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ilarity 34.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 396; DB 4; Length 657; Pred. No. 1.60e-74; 64; Mismatches III; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 398: DB 14: Length 259;
Pred. No. 4.65e-75;
39; Mismatches 104; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F4AB5238 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 657;
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ACCOMPANDATION ACCOMP
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O1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
HOMOLOG OF VACCINIA VIRUS CDS C3L.
        MASSUNG R.F., LOPAREV V.N., KNIGHT J.C., CHIZHTKOV V.E., TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases. EMBL; L22579; AAA60760.1; - EMBL; U18340; AAA69423.1; - EMBL; D1998; 1VVC.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BANGLADESH-1975;
MEDILINE; 94088747.
MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
MASSUNG R.F., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;
"Potential, virulence determinants in terminal regions of varid
                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-SOMALIA-1977;
                                                                                                                                                                                                                                                              smallpox virus genome.";
Nature 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variola virus.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orthopoxvirus
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Q9YTQ8;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT CONTROL PROTEIN HOMOLOG CCPH.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 CKSPDVINGSPISQKIIYKENERF-QYKCNMGYEYSERGDAVCTESGWRP-LPSCE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 CKIPOVANGHVEVRKTSNNVQYQYVNIKCDKGFRLQGETPNMCKNGVWFPALPTCE 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 ANGT--HTNIK-E-YYTYLDAVTYSCNDETKLTLTGPSSKOCSETGRWVPDEETKCEFKV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=73
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82; Conser
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                                                                                                                                                                                                                                                                                                             terminal regions of variola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 360;
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                                                                                                                                                                 SHCHELKUNOV S.N., TOTMENIN A.V.;
"Two types of deletions in orthopoxvirus
Virus Genes 9:231-245(1995).
EMBL; X69198; CAA40953.1; -.
PIR; C36838; C36838.
PIR; C36838; TVVC.
HSSP; P10998; TVVC.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
                                                                                                                                                                                                                                                                                                                         SHCHELKUNOV S.N., BLINOV V.M., RESENCHUK S.M., TOTMENIN A.V., OLENINA L.V., CHIRIKOVA G.B., SANDARKCHIEV L.S.; OLENINA to f the nucleotide sequence of 53 kbp from the right of the genome of variola major virus strain India-1967."; Virus Res. 34:207-236(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.; "Genes of variola and vaccinia viruses necessary protective mechanisms."; FEBS Lett. 319:80-83(1993).
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STRAIN=INDIA-1967, SSP. MAJOR;
MEDLINE; 93202281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variola virus
Viruses; dsDN
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D12L.
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STRAIN-INDIA-1967, SSP. MAJOR;
MEDLINE; 95320969.
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
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                                                                                      / Match 17.6%;
Local Similarity 33.6%;
nes 79; Conservative
 97
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                                                       40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
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 LDI-GG-V-DFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS 153
                             SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                              PF00084; sushi; 4
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                                                                                                                                                263 AA;
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                                                                                                                                                  28789 MW;
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Pred. No. 3.96e-64;
38; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
                                                                                    Score 357; DB 14;
Pred. No. 3.96e-64;
38; Mismatches 95
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                                                                                          Indels 23;
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Q89076;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q22328;
Q22328;
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HSSP, P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variola virus
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOH
                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                         STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                   COSMID T07H6
                                                                                                                                                                                                                                                                                                            T07H6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 KSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 KSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 PYPTILNGYLSSGFKRSYSYNDNVDFTCKYGYKLSGSSSSTCSPGNTWQPELPKC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 LDI-GG-V-DFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-Y-RECDTDG--WTNDIPICEVVKC-LPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IS-NGR--HNGYN-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WSNP-PTCQIVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHPTILNGYLSSGFKRSYSYNDNVDFTCKYGYKLSGSSSSTCSPGNTWQPELPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IS-NGR--HNGYN-DF-YTDGSVVTYSCNSGYSLIGNSGVLCSGGE-WSNP-PTCQIVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-Y-RECDTDG--WINDIPICEVVKC-LPVT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sushi; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.5%;
33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28842 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01,
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12,
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                                                                                                                                                                                                                               Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.34e-63; 38; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 355; DB 14;
Pred. No. 1.34e-63;
                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D66A9287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
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                                                                                           X
                 JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                    COULSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
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RESULT IN THE PROPERTY OF THE 
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Best Local
                                                                                                                                 EMBL; U75654; AAC13888.1;
HSSP; P10998; 1VVC.
PFAM; PF00084; sushi: 7
                                                                                                                                                                                                                                                                                FOSTER J.A., FRIDAY B.B., MAULIT M.T., BLOBEL C., WINFREY V.P., OLSON G.E., KIM K.S., GERTON G.L.;
"AM67, a secretory component of the guinea pig sperm acrosomal matrix, is related to mouse sperm protein sp56 and the complement component 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TREMBLREL. 12, Last annotation update)
ACROSOMAL MATRIX COMPONENT AM67 PRECURSOR.
Cavia porcellus (Guinea pig).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
      SEQUENCE
                                                                                                                                                                                                                                  binding proteins.";
J. Biol. Chem. 272:12714-12722(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97284752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-HARTLEY; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          008569;
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U53344; AAA96225.1; -.
HSSP; P10998; IVVC.
PFAM; PF00084; sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTWING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROPERA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 CDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 SKAKCMEDGQWSAPIPRCLA-SCRVPHIQNG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AQWFGPD-LR-CKARACPDPGDIENG---LREGDTFEYPHHVKYSCNPGFLLVGSTS-RQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 CSSNGEWTNEPANCKATECSRPSSPLHGKVVGSSL-T---YQ-S-VVTYSCDHGYRLVGQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 17.4%;
Local Similarity 32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQRICLAEGIWGGNEPRCEEIRCSVLPTLPNGYIEGSETSFGAVAVFRCLETMTHE-GA- 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDAVCTESG-WR-PLPSCEEKSCDNPYIPNG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEMHCSDDGFWSKEKPKCVEISCKS-PDVINGSPISQKIIYKENERFQYKCNMGYEYSER
533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     560 AA;
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                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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   59772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Mismatches 82; Indels 19;
                    POTENTIAL.

ACROSOMAL MATRIX COMPONENT AM67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 353; DB 5;
Pred. No. 4.52e-63;
60EEA526 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 AA
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ID QSE
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Best Local Similarity 27.0%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-CONGO-1965;

MASSUNG R.F., LOBAREV V.N., KNIGHT J.C., CHIZHIKOV V.E., PARSONS J.M.,

TOTMENIN A.V., SHCHELKUNOV S.N., ESPOSITO J.J.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

EMBL; U18337; AAA69317.1; -.

HSSP; P10998; IVVC.

PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q89061;
Q89061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variola virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                             133 APENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC
193 KSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                207 PHPTILNGYLSSGFKRSYSYNDNVDFTCKYGYKLSGSLSSTCSPGNTWQPELPKC 261
                                                                                                                                                                                                                                                                                                  78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-Y-RECDTDG--WINDIPICEVVKC-LPVT 132
                                                                                                                                                                                                                                                                                                                                                                           97 LDI-GG-V-DFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEKS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 IIT-DLL-FGSTIEFSCSKGYSLIGSTT-SQCESQGKTVDWSDFLPECVIVKCDSPPDIS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGW-TL--FNQCIKRRCPSPRDIDNGH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 C-DNPYIP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 CIDLPEVP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                 IS-NGR--HNGYN-DF-YTDGSVYTYSCNSGYSLIGNSGVLCSGGE-WSNP-PTCQIVKC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGK-HSGT-DEDL-YTYGSLYTYVCDPNYSLLGNASISCLVANKTYGVWSSNPPTCEKVI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKCLPVTAPE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETNFRTGTALKYNCHRGYWRVNSSHVICDINGSWI-YNVF--CAKKRCRNPGELANGKVE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRQPHIPKGIFLSGFGFYYTYKDTLVISCKKGYILRGSSIIHCEANSKWYPSIPTCEPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHC--SDD--GFWSKEKPKCVEIS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.28;
33.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 350; DB 14; Length 263; Pred. No. 2.81e-62; 37; Mismatches 96; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 351; DB 11; Length 533; Pred. No. 1.53e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55866165 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps 16;
                                                                                                                                                 192
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Job time: 30 secs.

8 21:43:01 2000

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Thu Jun 8 21:44:51 2000; MasPar time 11.39 Seconds 684.453 Million cell updates/sec

Description: Perfect Score: >US-09-316-163-11 (1-329) from US09316163.pep 2539

Sequence: 1 EDCNELPPRRNTEILTGSWS......PDIKHGGLYHENMRRPYFPV 329

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Watch 0% Lighting first 45 summaries

1-geneseq36

Database:

Mean 33.142; Variance 124.795; scale 0.266

Statistics:

pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	ഗ	4	ω	2	_	Result No.
395	397	398	398	399	399	399	399	399	400	402	403	404	406	406	409	409	409	409	433	452	1650	1832	Score
	15.6	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.8	15.8	15.9	15.9	16.0	16.0	16.1	16.1	16.1				65.0		Query Match
543	543	543	543	543	543	543	543	543	543	543	543	543	2039	1537	2317	1930	778	290	581	578	216	240	Length
μ	_	L	ш	_	-ـــا	سر	L	<u>_</u>	ᆫ	_	<u>, .</u>	ப	Ц	<u>,_</u>	ب	ب	Н	ᆫ	μ	$\vdash$	<b>,</b>	L	DB
R28567	R28565	R28555	R28558	R28568	R28571	R28547	R28569	R28552	R28550	R28560	R28557	R28553	R11810	R11982	P92219	W45899	W73147	W39156	R13490	Y09065	W39155	W39154	ID
CR1-4 (318-321 RNPP) a	-4 (	CR1-4 (92T) analogue.	CR1-4 (109N, 110A, 111	-4 (347T, 349Y)	-4 (364-36	-4 (52S, 53)	-4 (369-3	CR1-4 (78T, 79D) analo	CR1-4 (64K) analogue.	-4 (	-4 (	`	lement	Partial human compleme	CR1 protein	Human complement recep	Amino acid sequence of	ial compl	Human C4 binding prote		H410	=	Description
1.25e-29	7.61e-30	.95e-3	u	.65e-3	.65e-3	.65e-	.65e-3	ı L	.64e-3					. 29e	.96e	3.96e-31	, e	- 1	1.05e-33	9.41e-36	.47e-1	e-1	Pred. No.

Ş В QΥ

61 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 120

В

Query Match 72.2%; Score 1832; DB 1; Length 240; Best Local Similarity 100.0%; Pred. No. 3.40e-190; Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps

0,

В

4.4 4.5	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	1
362 341	371	376	382	382	385	385	386	387	389	391	390	391	393	393	393	393	394	394	395	395	
14.3 13.4	14.6	14.8	15.0		15.2	15.2	15.2		15.3	15.4	15.4	15.4	15.5	15.5	15.5	15.5		15.5.	15.6		
579 302	263	830	577	543	543	543	543	543	543	2039	543	543	543	543	543	543	543	543	543	543	
$\mu \mu$	1	Н	<b></b> -	H	Н	سر	М	Н	Н	۳	۲	۳	۳	Н	<b>-</b>	سر	_	Н	۳	٢	
W39924 R55793	P92003	R65216	W06882	R28546	R28559	R28543	R28554	R28556	R28564	R36743	R28548	R28544	R28562	R28570	R28566	R28545	R28551	R28561	R28563	R28549	
Amino acid sequence or Herpesvirus saimiri sC	Deduced sequence of co	P-selectin.	Membrane co-factor pro	CR1-4 (44T, 47D, 49L)	-4 (114-1	-4 (35E, 37Y) ana	-4 (92T, 94H)	) anal	CR1-4 (116K, 117P) ana	•	CR1-4 (57V, 59K) analo	-4 (35E) ana.	-4 (116K)	-4 (	-4 (	-4 (37Y) a	-4 (65T)	_	-4 (	4 (64K	
4.05e-25 6.77e-24	4.50e-27	1.32e-2/	3.04e-28	3.04e-28	.45e-2	1.456-28	1.14e-28	) N	.44e-2	.33e-2	. 266-2		.04e-2	.04e-2	2.04e-29	.04e-2	1.59e-29	1.59e-29	1.25e-29	1.25e-29	

SQ	88	86	38	င္ပ	Sd Sd	PT	ΡŢ	ΡŢ	DR	DR	ΡŢ	PA	PR	PR	PR	PR	PF	PD	PΝ	SO	ΧV	XV	7 5	1	AC t	RESULT
the manufacture of a medicament for the treatment of a tumour cell. Sequence 240 AA;	treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in	such proteins and a CFH antigens can be used in screening or for the	in the identification of complement factor H related proteins and	tumour-associated complement factor H (CFH). This sequence is used	This partial protein sequence represents a region of the human	H related antigen, or nucleic acid encoding it	by modulating or detecting tumour associated human complement ractor	Treating or screening for cancer, e.g. renal or urogenital cancer	N-PSDB; V02790.	WPI; 97-512742/47.	Enfield DL, Hass GM, Kinders RJ;	(BARD-) BARD DIAGNOSTIC SCI INC.	06-MAR-1997; US-038614.	09-APR-1996; US-630048.			09-APR-1997; U05710.		WO9738136~A1.	Homo sapiens.	urogenital cancer; medicament; modulator.	Complement factor H; tumour associated antigen; renal cancer;	Himan partial Complement factor H protein fragment 1.	1998		urgisa standard: Protein: 240 AA.

of

probe

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RESULT
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AC WAS
A
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09-APR-1997; UUS-812481.

06-MAR-1996; US-812481.

09-APR-1996; US-015083.

09-APR-1996; US-030048.

06-MAR-1997; US-038614.
                                                                                                                                                                                            06-JUL-1999 (first entry)
Human complement factor H homolog protein.
Human complement factor H; immunological mechanism; complement reaction;
gene therapy; immune stimulation; haematopoiesis regulation; chemotactic;
tissue growth activity; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating or screening for cancer, e.g. renal or urogenital cancer by modulating or detecting tumour associated human complement Factor H related antigen, or nucleic acid encoding it Example 6B; Fig 6B; 104pp; English.

This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour-associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                                               Y09065 standard; Protein; 578 AA.
                          15-APR-1999.
02-OCT-1998;
                                                                                                                                                                     secretory signal.
                                                                                                   WO9918200-A1.
                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                   Y09065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-1998 (first entry)
Clone pRRB9FH410 CFH related protein fragment.
COmplement factor H; tumour associated antigen; renal cancer;
urogenital cancer; medicament; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a medicament for t
Sequence 216 AA;
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N-PSDB; V02791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 QCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVRFVCNSGYKIEGDEEMHCSDDGFWGKEKPKCVEISCKSPDVINGSPISQKIIYKENER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENER 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGL 240
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Similarity 99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1650; DB 1; 1
Pred. No. 1.47e-169;
'Wismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
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   RESULTION RESULT RESULTION RESULT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        short consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human C4 binding protein.
C4bp; monomer; complement protein; pJOD.C4bp.3; SCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA encodes a protein having homology to human complement factor H, which plays a role in the immunological mechanism involving the complement reaction. The protein can also be used as an antigen for preparing antibodies against the protein. The cDNA can be used as a probe for gene diagnosis and the gene for gene therapy, as well as for large-scale expression of the protein. The protein may also have immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, anti-inflammatory activity, tumour inhibition activity, chemotactic/chemokinetic activity receptor/ligand activity, etc. The protein is identified by the presence of a hydrophobic N-terminal secretory signal region, knowledge of the protein function is not required, as in e.g. methods of expression
                                                                                                                                                                                        region
                                                                                                                                                                                                                                                         region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R13490 standard; Protein; 581 AA. R13490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Human proteins with secretory signal sequences and nucleotide sequences, useful in control of proliferation and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SAGA) SAGAMI CHEM RES CENT. Kato S, Sekine S; WPI; 99-264019/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 ENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claims 1; Page 55-58; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-1997; JP-272837. (PROT-) PROTEGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 ENTRRPYFPV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 LRIK-HRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRC-TLKPCDYPDIKHGGLYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 WFKLHDTLDYECYDGYESSYGNTTDSIVCGEDGWSHLPTCYNSSESCGPPPPISNGDTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 HFGQAVRFYCNSGY-KIEGDEE--MHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 ILNEETQYNCKPGYATADGNSSGSITCLQNG-WSTQ-PICIKF-CDMPVFENSRAKSNGM 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 YTCNEGYQLL-GEI-NYRECDTDGWTNDIPICEVVKCL-PVTAPENGKIVSSAMEPDREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 YYCDQNFVTPSGSYWDYIHCTQDGWSPTVP-C-LRTCSKSDVEIENG-FIS---ESSSIY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 17.8%;
Local Similarity 32.8%;
Local Similarity 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYKENERFQYKCNMGYE--YSERGDA-VCTESGWRPLPSC-EEK-SCDNPY-IPNGDYSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat.
                                                                 220. .279
/label= scr5
/label- SCR4
                                                                                                                                          156. .219
/label= scr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  'label= C4bp
83. .93
                                                                                                                                                                                                                                                                                            'label= SCR8
                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= signal_peptide
                                                                                                                                                                                                                       label= SCR7
                                                                                                                                                                                                                                                         .155
                                      . 345
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Pred. No. 9.41e-36;
56; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 578;
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proved binding protein fusion proteins and DNA encoding them -
proved binding protein fusion proteins and therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-1990; US-470888.
(BIOG-) BIOGEN INC.
W39156 standard; Protein; 290
W39156;
27-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 VEIKT-DL-SFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPDI 165
                                                                                                                                                                                                                                                                                                                                      191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.1%;
Local Similarity 29.8%;
les 97; Conservation
                                                                                                                                                                                           342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTFCIY-KR-CRHPGELRNGQ 107
                                                                                                                                                                                      QGCEALCCPEPKLNNGEITQHRKSRP 367
                                                                                                                                                                                                                                                                                                                            SCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYR-EC-DTD-GWINDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                   TCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPSPPACEPN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS-D-D--GFWSKEKPKCVEI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNGR--HSG-E-ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKI 221
                                                                                                                                                                                                                                                                                   SCINLPDIPHASWETYPRPTKEDVYVVGTVLRYRCHPGYKPTTDEPTTVICQKNLRWTPY 341
                                                                                                                                             PRCTLKPCDYPDIKHGGLYHENMRRP
                                                                                                                                                                                                                                      SCDN-PYIPNG--D-YS-PLRIK-HRTGDEITYQCRNGFYPATRGNTA-KC-TSTGWIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...406
/label= sr:
407
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524
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/note= "responsible for multimer assembly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 433; DB 1; Le
Pred. No. 1.05e-33;
68; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This partial protein sequence represents a region of the human the tumour-associated complement factor H (CFH). This sequence is used in the identification of complement factor H related proteins and antigens from clone prassprey210 (see W39157-W39159). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.

Sequence 290 AA;
                                                                                                                                                                                                                                                                                                   LT 6
W73147 standard; protein; 778
W73147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating or screening for cancer, e.g. renal or urogenital cancer by modulating or detecting tumour associated human complement Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BARD-) BARD DIAGNOSTIC SCI INC-
Enfield DL, Hass GM, Kinders RJ
WPI; 97-512742/47.
N-PSDB; V02792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1996; US-630048
06-MAR-1997; US-038614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1997; U05710.
06-MAR-1997; US-812481
09-APR-1996; US-015083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human partial complement factor H protein fragment 2. Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H related antigen, or nucleic acid encoding it Example 6B; Fig 7B; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             urogenital cancer; medicament; modulator.
                                                                                                                                                                   29-JAN-1999 (first entry)
Amino acid sequence of the soluble complement receptor 1 (sCR1).
Human; soluble complement receptor 1; sCR1; T-cell; B-cell;
mediated immune response; inhibition; tissue rejection; gene therapy;
mediated immune response; inhibition; tissue rejection; gene therapy;
dystrophin; inflammatory response; interferon-gamma secretory response;
autoimmune response; neurological response; Alzheimer's disease;
parkinson's disease; multiple sclerosis; systemic lupus crythematosus;
                                                                                             Homo sapiens.
WO9845430-A1.
                                      06-APR-1998; G01012.
05-APR-1997; GB-006950.
                                                                                                                                 rheumatoid arthritis; myasthenia gravis; epidermis bullosa;
Hashimoto's disease.
  (CHER/)
                    (ANNE/) ANNENKOV A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEGFGIDGPAIAK-CLGEKWSHP-PSCIKTDCLSLPSFENA-IPMGEKK-D-VYKAGEQV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYTCATYYKMDGASNVTCINSR-WT-GRPTCRDTSCVNPPTVQNAYIVSRQMSKYPSGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEGYOLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SSVEYQCQN-LYQLEGNKRITCRNGQWSEPPKC-LHPC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQYKCNMGYE-YSERGDAVCTESGWRPLPSCEEKS--CDNPY-IPNGDYSPLRIK-HRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRYQCRSPYEMFGD-EEVMCLNGNWTEPPQCKDSTGKCGPPPPIDNGDITSFPLSVYAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC-KSPDVINGSPIS-QKIIYKENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.1%;
Similarity 27.0%;
    CHERNAJOVSKY Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hass GM, Kinders RJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 409; DB 1;
Pred. No. 3.96e-31;
63; Mismatches 119
                                                                                                                                                                                                                                                                                                                                 B
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Best Local
                                                                                                       22-JAN-1998.
08-JUL-1997; E03715.
15-JUL-1996; GB-014871.
(ADPR-) ADPROTECH PLC.
DODD I MOSSAKOWSKA DEI, Smith RAG;
WPI; 98-110524/10.
Derivatives of soluble poly:peptide(s) bonded to low affinity membrane binding groups - useful for treating complement-relation thrombotic diseases, providing improved localisation at cellu:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human complement receptor 1 (residues 1-1929).

Membrane binding element; thrombotic disease; soluble protein;
complement-related disease; integral membrane protein; inflammation;
short consensus repeat; SCR 1-3; CR1; complement receptor type 1.
                                                                                                                                                                                                                                                                                                                                 WO9802454-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross_links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W45899 standard; peptide; 1930 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W45899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory responses such as rheumatoid arthritis
Disclosure; Fig 1, 54pp: English.
This is an amino acid sequence of the human soluble complement receptor 1 (sCR1), useful in the treatment of T-cell or B-cell mediated immune responses. It is used to inhibit a T-cell or B-cell-mediated immune response to prevent immune response-mediated tissue rejection and destruction or clearance or inactivation of an expressed protein especially from cells that have been treated by gene therapy to express the protein, e.g. dystrophin. The protein can also be used to inhibit a T-cell or B-cell-mediated inflammatory response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an interferon-gamma secretory response, autoimmune response or neurological response, e.g. Alzheimer's or Parkinson's disease or multiple sclerosis. Also the protein can be used to treat systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, epidermis bullosa or Hashimoto's disease.

Sequence 778 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annenkov A, Chernajovsky Y; WPI; 98-568350/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMVHVIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
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Local Similarity 31.48;
es 97; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
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                                                                                                                                                                                                                                                                                                                          /note= "Disulphide linked to Cys in peptide given in W45889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 3.96e-31;
           ul for treating complement-related 
improved localisation at cellular
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CC N-terminal fragment. The invention relates to a soluble derivative (A)
CC of a soluble polypeptide (I), which comprises at least 2 heterologous
CC membrane-binding elements (MBE) of low membrane affinity covalently
CC additivity, with components of cellular or artificial membranes exposed
CC of a covalent of the components of cellular or artificial membranes exposed
CC (I) itself, specifically inflammation or any other complement-related
CC disorder (e.g. neurological disease, graft rejection, myocardial
CC disorder (e.g. neurological disease, but also to
CT treat allergy, induce weight loss, to treat ischaemia or asthma and as
CC treat allergy, induce weight loss, to treat ischaemia or asthma and as
CC treat allergy, induce weight loss, to treat ischaemia or asthma and as
CC orally, topically, by injection or inhalation at 0.01-10 (preferably
CC 0.1-10) mg/kg/day.
SQ sequence 1930 AA;
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Best Local
for diagnosis and control of complement-related immune defects, inflammation, myocardial infarct, etc Claim 1; fig. 1; 191pp; English.
This is full-length CR1 protein, and shortened forms are new, lacking the transmembrane region. The proteins and fragments bind C3b and/or
                                                                                                                      New nucleic acid sequences encoding new CR1 protein - and its fragment
                                                                                                                                                                            Ol-APR-1988; US-176532.
(TCEL) T Cell Sciences Inc; (UYJO) The Johns Hopkins University; (BRIG*) The Brigham and Women's Hospital.
Fearon DT, Klickstein LB, Wong W, Carson G, Concino MF, Makrides WPI; 89-309498/42.
                                                                                                                                                           N-PSDB; N91477
                                                                                                                                                                                                                                                                                                05-OCT-1989.
31-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                 WO8909220-A.
                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complement; cofactor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR1 protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P92219 standard; protein; 2317 AA. P92219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1990
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Claim 22; Pages 60-61; 75pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 IVSSAMEPDREYHFGQAVRFYCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSTYCTSNDDQVGIWSGPAPQCI 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMVHVIK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG
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Local Similarity 31.48;
es 97; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                             10. .50
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Pred. No. 3.96e-31;
66; Mismatches 110
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Best Local
            18-APR-1991.
25-SEP-1990; US-412745.
26-SEP-1989; US-412745.
26-SEP-1990; US-912349.
(TCEL-) T CELL SCI INC.
(UJO) JOHNS HOPKINS UNIVERSITY.
(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
FEATON DT, Klickstein LB, Wong WW, Cars Markides SC, Marsh HC;
WPI; 91-132854/18.
N-PSDB; Q11643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4b, have cofactor activity and inhibit C3 and C5 convertase activity. In the sequence, x-untranslated region. This has 7 short consensus repeats (CR) of 4 long direct homologous repeats (LHR) (see fig. 10 in patent). Deletion mutants, eg LHR-A for binding of C4b, and LHR-C for C3b binding, be made, and LHR-B and -C can detect CR2 sequences. They are useful in diagnosing and treating immune disorders, and prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                perfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                           Partial human complement type 1 receptor. complement system; C3b/C4b receptor; CR1; allergic
                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R11982 standard; Protein; 1537 AA
                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1991
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                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                  lmmune response; long homologous repeat; LHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189
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nes 97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMVHVIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTCEVKSCD 368
 complement receptor type 1 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.1%;
larity 31.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                     1521. .1526
/note= "has 67 per cent homology to kinase C phosphorylation in the EGF receptor"
                                                                                                                                                                                                                                                   1495. .1498
/note= "positively-charged; preceded sequence"
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           'label-
                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                               'label=
                                                                                                                                                                                                                                                                                                            .1341
                                                                                                                                                                                                                                                                                                                                         .891
                                                                                                                                                                                                                                                                                                                                                          LHR-B
                                                                                                                                                                                                                                                                                               LHR-D
                                                                                                                                                                                                                                                                                                                          LHR-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 409; DB 1;
Pred. No. 3.96e-31;
66; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 110; Indels 36;
                                                            Carson
   encoded proteins
                                                            GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2317;
                                                            Hoh
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                                                             Concino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
  Query Match 16.0%;
Best Local Similarity 28.8%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure: Fig 5; 234pp; English.

This sequence comprises three of the four tandem, direct, long this sequence comprises three of the Inogth F allozyme of CR1. LHR-A is homologous repeats of the full-length F allozyme of CR1 of Short absent. Each LHR might represent a single C3b/C4b binding domain, making the receptor multivalent. The LHR's are composed of 7 short consensus repeats of 60-70 residues resembling the SCR's of other C3/C4 binding proteins. The protein and fragments of it having C3b and/or C4b binding activity can be used to treat immune disorders and of C4b binding activity can be used to treat immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also Q11642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments - for treatment of immune disorders, myocardial infarct, damage due to inflammmation and in treatment of thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or disorders involving inappropriate complement activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1202 PRCTVKSCD 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1085 STNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQPGFVMVGSHTVQCQTNGRWGPKLPHC 1144
              Human complement receptor type 1 gene, encoded proteins and fragments - for treatment of immune disorders, myocardial in damage due to inflammmation and in treatment of thrombosis Claim 41; Fig 1; 234pp; English.
                                                                                                                            (TCEL) T CELL SCI INC.
(UYJO) JOHNS HOPKINS UNIVERSITY.
(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
FEATON DT, KILCKSTEIN LB, WONG WW, Ca
Makrides SC. Marsh HC;
                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human complement type 1 receptor; complement system; C3b/C4b receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           969
                                                                                                                                                                                                                              18-APR-1991.
25-SEP-1990; U05454.
26-SEP-1989; US-412745.
26-SEP-1990; US-912349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R11810 standard; Protein; 2039 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   914 FPVGTSLNYECRPGY--FGKMFSISCLENLVWSSVED--NCRRKSCGPPPE-PFNGMVHI 968
                                                                                               N-PSDB; Q11642.
                                                                                                                                                                                                                                                                                                             WO9105047-A.
                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response; clone lambda T109.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1991 (first entry)
The invention also covers fragments of this protein which have the
                                                                                                                  WPI; 91-132854/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 PRCTLKPCD 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-RVCQPPPEILHGEHTLSHQDNFSPGQEVFYSCEPS-Y-DLRGAASLHCTPQGDWSPEA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIS-CKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYSNUR-TS--FHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSPPPRCI 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGNVFEYGVKAVYTCNEGYQLLGE--INYRECDTD-GWTNDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGTFTLT
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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12. .2039
                                                                                                                                                                                                                                                                                                                                    CR1
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                                                                                                                                                        Carson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR1; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                        GR,
                                                                                                                                                          Hoh
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                                                                                                                                                             Concino MF
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Best Local Similarity 28.8%;
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for diagnosis etc.

Claim I1; Fig 2 and R11810; 23pp; English.

The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988)

168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of
                                                                                                                     03-MAY-1991; US-695514.
(UNIW ) UNIV WASHINGTON.
Atkinson JP, Hourcade D, Krych M;
WPI; 92-375009/46.
                                                                                   Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant reject
                                                                                                                                                                                                                                                           misc_difference
                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-1993 (first entry)
CR1-4 (85R, 87N) analogue.
short consensus repeat; regulator of complement activation; c3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                       28-APR-1992; 303826
                                                                                                                                                                                                                          EP-512733-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ability to bind C3b and/or C4b, have cofactor I activity or can inhibit C3 or C5 convertase activity. The full-length protein, or its specified fragments are used to treat patients with immune disorders or a disorder caused by inappropriate complement activity. The protein is also used to treat thrombotic conditions in humans and animals. See also Q11643.
                                                                                                                                                                                                                                                                                                                                                                                                                                          region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R28553 standard; peptide; 543 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 PRCTLKPCD 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIS-CKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STNKCTAPEVENAIRVPGNRSFFSLTETIRFRCQPGFVMVGSHTVQCQTNGRWGPKLPHC 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYSNNR-TS--FHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSPPPRCI 1586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGTFTLT
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                                                                                                                                                                                                                                                                                          /note=
85
                                                                                                                                                                                                                                                       /note= "Gln substituted by Arg (SCR-9)"
87
                                                                                                                                                                                                                                    /note= "Lys substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                         /label= SCR-8
                                                                                                                                                                                                                                                                                                                                                                                                                         'label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                         'label= SCR-2
                                                                                                                                                                                                                                                                                                                                         .543
                                                                                                                                                                                                                                                                                                                                                                                                         .122
                                                                                                                                                                                                                                                                                                                                                                      .510
                                                                                                                                                                                                                                                                                                     "TRUNCATED"
                                                                                                                                                                                                                                                                                                                           SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 406; DB 1; Length 2039; Pred. No. 8.29e-31; 70; Mismatches 114; Indels 36;
                                                                                    rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local
treating auto:immune diseases, to suppress transplant for diagnosis etc.
Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                   (UNIW ) UNIV WASHINGTON. Atkinson JP, Hourcade D, WPI; 92-375009/46.
                                                                                   Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                          28-APR-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                          EP-512733-A.
11-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-1993 (first entry)
19-MAR-1993 (first entry)
CR1-4 (99H, 103E) analogue.
short consensus repeat; regulator of complement activation; short consensus repeat; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                    misc_difference 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R28557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R28557 standard; peptide; 543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 PRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 PTCEVKSCD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 FDIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMVHVIK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-I-QFGSRINYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.9%;
Similarity 31.1%;
96; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543 AA;
                                                                                                                                                                                                                             US-695514
                                                                                                                                                                                                                                                             303826
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= SCR-8
511. .513
                                                                                                                                                                                                                                                                                                                                          /note= "Thr substituted by Glu (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                    note= "Ser substituted by His (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCR-9
                                                                                                                                                                Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 404; DB 1; Length 543; Pred. No. 1.36e-30; 67; Mismatches 110; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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PPR DR BE BE PRACE OF THE PRACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CRI-4 sequence; the sequence given here was constructed from the full-length CRI amino acid sequence having GENESEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                 11-NOV-1992.
28-APR-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRI-4 (1145) analogue.
short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R28560 standard; peptide; 543 AA.
                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                     Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant reject
                                                                                                        Atkinson JP, Hourcade D, Krych M; WPI; 92-375009/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
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                                                                                                                                                                               (UNIW ) UNIV WASHINGTON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 APTCEVKSCD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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   diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CS-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-I-QFGSQIKYSCTKGYRLIGHSS-AECIISGDTVIWDNETPICDRIPCGLPPTIT-NG 134
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                                                                                                                                                                                                                    303826.
US-695514
                                                                                                                                                                                                                                                                                                                                                                                                /label = SCR-9
/note = "TRUNCATED"
114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= SCR-8
511. .543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              /note= "Asp substituted by Ser (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= SCR-2
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Pred. No. 1.74e-30;
67; Mismatches 108
                                            to suppress transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 108; Indels 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEO accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 2 and R11810; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                           region
                                                                                                                                                                                                                                                                                                                                                               CR1-4 (64K) analogue.
short consensus repeat; regulator of complement activation;
c3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                           region
                                                                                                                                                                                                                                                                                                                                                                                                               R28550;
19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                               R28550 standard; peptide; 543 AA
                             Atkinson JP, Hourcade D, WPI; 92-375009/46.
                                                                            11-NOV-1992.
28-APR-1992; 303826.
03-MAY-1991; US-695514
 Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection.
                                                                                                                                                               misc_difference
                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.8%;
Local Similarity 31.1%;
hes 96; Conservation
treating auto:immune
                                                              (UNIW ) UNIV WASHINGTON
                                                                                                                                EP-512733-A.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-@GWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWSNETPICDRIPCGLPPTIT-NGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTCEVKSCD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                          /note= "TRUNCATED"
                                                                                                                                                                                                                                               451.
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                               /label= SCR-2
451. .510
                                                                                                                                                /note= "Arg substituted by
                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                              /label= SCR-1
                                                                                                                                                                                                                .543
                                                                                                                                                                                                                                SCR-8
                                                  Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 402; DB 1;
Pred. No. 2.22e-30;
67; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                    useful
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RESULTIAN ACTION ACTION
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Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810 and descriptions in J.Exp.Med.(1988)

Claim 12; Fig 2 and R11810 and descriptions in J.Exp.Med.(1988)

Claim 12; Fig 2 and R11810 and descriptions in J.Exp.Med.(1988)

Claim 13; Fig 2 and R11810 and descriptions in Later Claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                        11-NOV-1992.
28-APR-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IT 15
R28552; standard; peptide; 543 AA.
R28552;
19-MAR-1993 (first entry)
CR1-4 (78T, 79D) analogue.
short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type 1 receptor.
   (UNIW ) UNIV
Atkinson JP,
                                                                                                                                                      EP-512733-A.
                                                                                                                                                                                                                                                                             misc_difference 78
                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 PRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 IVSSAMEPDREYHFGQAVRFYCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 PTCEVKSCD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
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                                                              303826.
US-695514.
WASHINGTON.
Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                              79
                                                                                                                                                                   /note= "Gly substituted by Asp (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                              note= "Lys substituted by Thr (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                   'note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= SCR-1
61. .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= SCR-2
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                                                                                                                                                                                                                                                                                                                                                            .510
'= SCR-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rfor diagnosis etc.

7 for diagnosis etc.

7 claim 11; Fig 2 and R11810; 23pp; English.

7 The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988)

7 close 1255-1270. It encodes the first 8 and a half amino terminal

8 close of CR1. The invention concerns analogues of "regulator of

9 complement activation" proteins or truncated, hybrid or recombinant

9 complement of them. CR1-4 is a preferred truncated form and a number of

9 complement of them. CR1-4 is a preferred truncated form and a number of

9 complement activation variants of it are claimed in which certain

9 complement of SCR-9 which have been identified as important for the

9 contain the CR1-4 sequence; the specification does not

9 contain the CR1-4 sequence the sequence have was constructed

9 contain the CR1-4 sequence; the sequence have was constructed

9 contain the CR1-4 sequence for a here was constructed

9 concession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
300
                                                310 PTCEVKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                 245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                                                          193 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                             139 IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV
                                                                                                                                                                                                                                                                                                                         136 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
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                                                                                                                                                                                                                                                                                                                                                                                                                       78 TDI-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPD-PVNGMYHVI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 15.7%;
Local Similarity 30.7%;
es 95; Conservative
PRCTLKPCD
                                                                                                                                                                                  EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                            S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 AA;
308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 399; DB 1;
Pred. No. 4.65e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
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Search completed: Thu Jun 8 21:45:07 2000 Job time : 16 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jun 8 21:45:24 2000; MasPar time 19.71 Seconds 787.259 Million cell updates/sec

Tabular output not generated.

Description: perfect Score: Sequence: >US-09-316-163-11 (1-329) from US09316163.pep 2539 1 EDCNELPPRRNTEILTGSWS......PDIKHGGLYHENMRRPYFPV 32

Scoring table: PAM 150 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Lighting first 45 summaries

pir62 (1:pir2 2:pir2 3:pir3 4:pir4

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 43.995; Variance 69.824; scale 0.630

Statistics:

#### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	a	σ	4	ω	N	1	Result
362	367	371	373	376	387	388	388	402	403	404	409	409	423	433	433	438	447	603	1236	1772	2539	2539	Score
14.3	14.5	14.6	14.7	14.8	15.2	15.3	15.3	15.8	15.9	15.9	16.1	16.1	16.7	17.1	17.1	17.3	17.6	23.7	48.7	69.8	100.0	100.0	Query Match
579	768	345	676	830	482	560	263	469	661	558	2489	2039	2014	597	303	452	597	1053	669	1234	1231	449	Length
Ν	N	دع	N	N	N	N	<u>سم</u>	Н	N	N	2	N	N	Ь	Ŋ	N	Ь	N	N	۳	ш	ш	DB
A56/40	I53821	NBMS	A45900	A30359	A34924	T16833	WMVZSP	NBMSC4	I36937	S57953	173012	A28507	I36936	NBHUC4	H35068	A35068	S53711	S46199	S65551	HSMEN	NBHUH	NBHUHS	ID
sperm-egg recognition	P-selectin - rat	-	complement C3b recept	P-selectin precursor		hypothetical protein	apolipoprotein H nomo	C4b-binding protein a	complement receptor 1	C4BP protein alpha ch	complement C3b/C4b re	complement C3b/C4b re	н	C4b-binding protein a	ein H-rei	complement factor H-r	C4BP alpha chain prec	probable complement r		nt lactor H	factor H	complement factor H p	Description
0.00	2.000-00	2.20e-61	/.21e-62	1.356-62	2.846-65	1.020-00	1.028-00	6.13e-69	3.49e-09	1.98e-69	1.18e-/0	1.18e-/U	4.250-74	1.45e+/6	1.456-70	8.450-78	OLE-8	2.98e-119	3./1e-284	0.00	0.00e+00	0.00e+00	Pred. No.

4.	44	43	42	41	40	<u>د</u> 9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
309	314	318	320	325	328	328	331	336	335	335	334	338	338	340	341	341	343	357	357	360	363
12.2	12.4	12.5	12.6	12.8		12.9	13.0	13.2	13.2	13.2	13.2	13.3	13.3	13.4	13.4	13.4	13.5	14.1	14.1	14.2	14.3
551	612	610	610	1091	369	362	345	497	384	377	345	369	349	661	360	302	768	610	263	808	668
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I46709	S23174	A32606	A35046	PL0009	JC5138	JC5194	NBHU	JC2054	S01896	I54479	NBBO	I57998	G02913	KFHU13	WMBE2E	WMBE1E	A42755	146001	C36838	D35069	A46013
endothelial leukocyte	endothelial leukocyte	endothelial leukocyte		0	membrane cofactor pro	membrane colactor pro	apolipoprotein H prec	complement regulatory	membrane colactor pro			membrane cofactor pro	sperm CD46 - numan (I	coagulation factor Al	membrane-bound compre	secretory complement	P-selectin precursor	C4b-binding protein a	complement control pr	ractor H	coagulation factor XI
1.58e-46	1.04e-4/	1.1/6-40	3.916-49	2.53e-50	4.0/6-01	4.070-61	9.3/6-02-	0.986-00	I. 040-02	1.046-52	1.806-04	1.996-00	1.996-00	1 000 5	C . / 90 - 54	3.790-04	1.200-54	0.5/d=50	5.376-50	I. O L E - L O	1,91e-59

an additional nucleotide present within the court for	##note	
	##residues	
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Dinding Sice	# 0000 to fo	
partial cDNA sequence of the 38 kpa cryptic reasurement		
Human complement factor H: 1501ation of cone croses and	#title	
(1986)	#journal	
	#auciors	
Schwlz TF: Schwaeble, W.: Stanley, K.K.; Weiss, E.;	REFERENCE ***********************************	
only portions of this i.e kilobase make were sequence	##note	
1-33;434-449 ##Label EST	##residues	
type	##molecule_	
not compared with conceptual translation	##status	
	#accession	
cross-references MUID:91184292	#cross-refe	
from alternatively spliced transcripts.		
Human complement factor H: two factor H proceins are derived	#title	
3	#journal	
Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.n.	#authors	
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mature protein was confirmed by protein sequencing		
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Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, K.B.	#authors	
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S03013; B60238; A27877; A61103; A26505; S10479	ACCESSIONS	
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complement factor H-related process; complement process "	ALTERNATE_NAMES	
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FEATURE
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Pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.
Biochemistry (1992) 31:3626-3634
#title Solution structure of the fifth repeat of factor H: A second #cross-references MUID:92232649
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##residues 226-T01,'Y',403-449 ##label KRI
##cross references GB.M12383; NID:9180472; PIDN:AAA52013.1; PID:9180473
WT Factor H has also been found bound to cell membranes in an unknown
manner. However, it has at least one cell attachment site motif
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27-76 ##label SC2
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19-20,'Q',22-29,'V',31-33,'Q',35 ##label SIM
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                                                                                                                                                                                                                                                                                                                         a cofactor in the inactivation of C3b by serine proteinase I;
                                                                                                                                                   alternative splicing; complement alternate pathway;
                                                                                                                                                                                                #superfamily complement factor H; complement factor H repeat
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Structural analysis of human complement protein H: homology with C4b binding protein, beta(2)-glycoprotein I, and the Ba fragment of B.
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Purification and structural studies on the complement-system control protein beta-1-H (factor H).
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Eur. J. Immunol. (1987) 17:1485-1489
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                                                                                                                                      glycoprotein;
                                                                                                                                                                                                                                                    convertase) in the alternative complement pathway
                                                                                                                                                                                                                                                                            also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5
                                                                                                                                                                                                                                                                                                                                                                                        indicated is unclear; factor H has been reported several allelic forms
#domain complement factor H repeat homology #label FH01\
                            #product complement factor H, short splice form #status
experimental #label MAT\
                                                                         #domain signal sequence #status predicted #label SIG\
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##cross-references_EMBL:Y00715; NID:g31964; PIDN:CAA68704.1; PID:g31965
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Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. (1991) 21:799-802
Human complement factor H: two factor H proteins are derived from alternatively spliced transcripts.
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#journal Biosci. Rep. (1987) 7:201-207

#title Sequence analysis of a cDNA clone encoding the C-terminal end conforman complement factor H.

#cross-references MUID:88025472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Ripoche, J.; Day, A.J.; Willis, A.C.; Belt, K.T.; Campbell, R.D.; Sim, R.B.
#journal Blosci. Rep. (1986) 6:65-72
Partial characterization of human complement factor H by protein and cDNA sequencing: homology with other complement and non-complement proteins.
#cross-references MUID:86188123
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#journal Biochem. J. (1982) 205:285-293
#title Purification and structural studies on the complement-system control protein beta-1-H (factor H).
#cross-references_MUID:83048213
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                                                                                                                                                                                                                                                                                            #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.;

pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.

#journal Biochemistry (1992) 31:3626-3634

#title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.

#cross-references MUID:922326649
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J. Immunol. (1991) 146:3190-3196
Cloning of the 1.4-kb mRNA species of human complement factor
H reveals a novel member of the short consensus repeat
family related to the carboxy terminal of the classical
150-kDa molecule.
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J. Mol. Biol. (1991) 219:717-725
Three-dimensional structure of a complement control protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norman, D.G.; Barlow, P.N.; Baron, M.; Day, A.J.; Sim, R.B.; Campbell, I.D.
  Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano.
                                                                                                                                                                                                                                                                                                                                                                                                                                annotation; NMR structure determination, residues 927-985
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#note the correspondence
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##residues 411-419;574-578,580-582 ##label CAR
#Factor H has also been found bound to cell membranes in an unknown
manner. However, it has at least one cell attachment site motif
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Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed
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Biochim. Biophys. Acta (1996) 1289:305-311
Factor H co-purifies with thrombospondin isolated from
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416-442,448-494, 477-505,509-553, 536-564,569-611, 597-623,630-673,

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901-926,931-973,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329;
          Natsuume-Sakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y. J. Immunol. (1990) 144:358-362
Demonstration of an unusual allelic variation of mouse factor
                                                                                                                                                                      Kristensen, T.; Tack, B.F.
Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3963-3967
Murine protein H is comprised of 20 repeating units, 61 amino acids in length.
                                                                                                                                                                                                                                                                                      protein beta-1-H

#formal_name Mus musculus #common_name house mouse
30_Sep-1987 #sequence_revision 30-Sep-1987 #text_change
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complement factor H precursor - mouse
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597-622,629-672,658-683,690-732,718-743,752-791,780-802,808-850,836-861,867-920,906-931,936-978,
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##residues 1-19 ##label RE2
##cross-references GB:J02891; NID:g193805; PIDN:AAA37795.1; PID:g553926
##cross-references GB:J02891; NID:g193805; PIDN:AAA37795.1; PID:g553926
NT Two codominant alleles of factor H are present in mice.
NT Factor H functions as a cofactor in the inactivation of C3b by serine proteinase I and also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) and the (C3b)nBb complex (C5
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Biochemistry (1989) 28:9891-9897
Analysis of complement factor H mRNA expression:
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476-530
                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Soames, C.J.; Day, A.J.; Sim, R.B.
#journal Biochem. J. (1996) 315:523-531
#title Prediction from sequence comparisons of residues of factor H
#title involved in the interaction with complement component C3b.
#cross-references_MUID:96202005
                                                                                                                                                                                                                                                                                                                                                                                                         #accession
                                                                                                                                                          599-651
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Local Similarity 65.7%;
local Similarity 65.7%;
                                                                                                                                                                                                                                                                                                                                                     ##residues
                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
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                                                                                Local
7 LAEGNQFEYGAKVVYTCDEGYQMVGEMNFRECDINGWINDIPICEVVKCLPVIEPENGKI 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLCEVVKCLPVTELENGRIVSGAAETDQEYYFGQVVRFECNSGFKIEGHKEIHCSENGLW 198
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Similarity 61.4%;
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                                                                                                                                      #length 669
                                                                Conservative
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                                                                                                                                      #checksum 8335
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Pred. No. 0.00e+00;
49; Mismatches 64; Indels
                                                              Score 1236; DB 2; 1
Pred. No. 3.71e-284;
35; Mismatches 59;
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#accession $46199
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##cross-references EMBL:L21703; NID
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##residues 526-532,'X',534-537;809-817,'X',819-826 ##label DAH2
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  141
                                    162 IGG--PE-EATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
                                                                                                                           103 AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQV 161
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                                                                                                                                                                      21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
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SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                    TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV 140
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Blochem. J. (1994) 301:391-397
Cloning and characterization of a cDNA representing a
putative complement regulatory plasma protein from barred
sand bass (Parablax neblifer).
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19_Mar-1997_#sequence_revision 06-Jun-1997 #text_change
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Pred. No. 2.98e-119
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                                                                                                                                                                                                                                                                                                                                                  NSCLGLPNVPHASQQGYQWSTKEGVYSVGTELRYKCRPGYRPVADEPIIVTCQEDLRWSP 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IICSPPNVPHGKIISGFGPIYNYKDSIMYTCIDGFVLRGSSLIHCELDSKWNPSPPVCES 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD--GFWSKEKPKCVE 189
                                                                                                                                                     APRCTLKPCDYPDIKHGGLYHENMRRP 325
                                                                                                                                                                                                                                                                                                                                                                                                                       ISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCT-ESGWRPLPS-CEE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDQTYPEGTQAIYKCRPGYRSLG-NVIMVCR-KGEWVALNPLRKCQKRPCGHPGDTPFGT 77
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Similarity 30.9%;
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Biochim. Biophys. Acta (1995) 1261:285-289
cDNA structure of rabbit C4b-binding protein alpha-chain.
Preserved sequence motive in complement regulatory protein
modules which bind C4b.
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C4BP alpha chain precursor - rabbit
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Pred. No. 5.01e-80;
62; Mismatches 133
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#journal J. Biol. Chem. (1990) 265:3193-3201
#title Identification and sequence analysis of four complement factor H-related transcripts in mouse liver.
#cross-references MUID:90153969
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                                                                                                                                                                    ##residues 1.303 ##label VIK
##cross-references GB:M29007; NID:g192557; PID:g309164; GB:J05259
##note translation of the nucleotide sequence is not complete
##IOTEATION #superfamily complement factor H repeat homology
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##cross-references GB:M29010; NID:g192561; PIDN:AAA37415.1; PID:g387128
##note translation of the nucleotide sequence is not complete
FICATION #superfamily complement factor H; complement factor H repeat
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Local Similarity 56.4%;
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apollipoprotein H-related protein 23L1 - mouse
#formal_name Mus musculus #common_name house mouse
27-Jul-1990 #sequence_revision 31-Dec-1993 #text_change
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Identification and sequence analysis of four complement
factor H-related transcripts in mouse liver.
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B.F.; Chaplin, D.D.
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Pred. No. 8.46e-78;
16; Mismatches 25
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#journal Biochem. Biophys. Res. Commun. (1989) 165:138-144
Molecular cloning of the cDNA coding for proline-rich protein
(PRP): identity of PRP as C4b-binding protein.
#cross-references_MUID:90073699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-597 ##label MA1
##cross-references GB:M31452; NID:g190501; PIDN:AAA36507.1; PID:g190502
##note the authors translated the codon GGA for residue 492 as
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                                                                                                                                                                                                                                                                                                                                                                                              ##residues 80-597 ##label CH2
##cross-references GB:X02865; NID:g29564; PIDN:CAA26617.1; PID:g29565
##note 92-Thr and 357-His were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 17-81 ##label LI2
##cross-references EMBL:X07853
##note although the sequence determined extends to residue 9
                                                                                                                              ##cross-references EMBL:X04284; EMBL:X04296
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Blochem. J. (1985) 230:133-141
Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.
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FEBS Lett. (1988) 232:328-332
Derivation of the sequence of the signal peptide in human
C4b-binding protein and interspecies cross-hybridisation of
the C4bp cDNA sequence.
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13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change
                                                                                                                                                                                                                                                                                      Lintin, S.J.; Reid, K.B.M. FEBS Lett. (1986) 204:77-81 Studies on the structure of the human C4b-binding protein
Rodriguez de Cordoba, S.; Sanchez-Corral, P.; Rey-Campos, J. J. Exp. Med. (1991) 173:1073-1082
Structure of the gene coding for the alpha polypeptide chain of the human complement component C4b-binding protein.
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#title
*JUMINAL J. Biol. Chem. (1988) 263:17034-17039

*title Binding site for vitamin K-dependent protein S on complement cross-references MUID:89034204

**ACCOSS-TEFETENCES MUID:89034204
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#title Genomic organization of the alpha chain of the human
#cross-references MUID:91113199
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Mol. Immunol. (1985) 22:427-435
Amino acid sequence studies of human C4b-binding protein:
N-terminal sequence analysis and alignment of the fragment
produced by limited proteolysis with chymotrypsin and the
peptides produced by cyanogen bromide treatment.
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The region Ser(333)-Arg(356) of the alpha-chain of human
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          #title Primary sequence of an alternatively spliced form of CRl.
Candidate for the 75,000 M(r) complement receptor expressed
on chimpanzee erythrocytes.
#cross-references MUID:94292799
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Local Similarity 29.8%;
hes 97; Conservative
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                                                                                 Birmingham, D.J.; Shen, X.P.; Hourcade, D.; Nickells, M.W.; Atkinson, J.P.
J. Immunol. (1994) 153:691-700
                                                                                                                                                                                                  I36936 #type fragment
complement receptor 1 - chimpanzee (fragment)
fformal_name Pan troglodytes #common_name chimpanzee
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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Pred. No. 1.45e-76;
68; Mismatches 132; Indels 29; Gaps
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                                                                                                                       ACCESSIONS
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#cross-references MUID:89035992
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                                                                                                                                                                                                                                                                                                                                                                        245 EEKSCDNP-YIPNGDYSPLRIKH-RTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIP-A
                                                                                                                                                                                                                                                                                                             300 PRCTLKPCD-Y-PDIKHG-GLYHENMR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GGNVFEYGVKAVYTCNEGYQLLGE--INYRECDTD-GWTNDIPICEVVKCLPVTAPENGK 138
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Similarity 29.1%;
                                                                                                                                                                                    A28507 #type complete
complement C3b/C4b receptor precursor, membrane-bound
(allotype F) - human
complement receptor type 1 (CR1); surface glycoprotein CD35
                    Klicketein, L.B.; Bartow, T.J.; Miletic, V.; Rabson, L.D.; Smith, J.A.; Fearon, D.T.
J. Exp. Med. (1988) 168:1699-1717
Identification of distinct C3b and C4b recognition sites in the human C3b/C4b receptor (CR1, CD35) by deletion
                                                                                                                         S03843; A28507; I56203; A24748; B24748; C24748
                                                                                                                                              #formal_name Homo sapiens #common name man
19-Nov-1988 #sequence_revision 06-Sep-1996 #text_change
10-Sep-1997
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Pred. No. 4.26e-74;
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616-682
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421-487
493-549
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104-161
166-232
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#map_position 1932-1932

#introns 41/1; 101/1; 134/2; 163/1; 296/1; 355/1; 389/2; 418/1; 491/1; 551/1; 584/2; 613/1; 746/1; 805/1; 839/2; 868/1; 941/1; 101/1; 1034/2; 103/1; 1196/1; 1255/1; 1289/2; 1318/1; 1001/1; 1034/2; 1063/1; 1196/1; 1255/1; 1289/2; 1318/1; 104/41; 1454/1; 1467/2; 1516/1; 1649/1; 1708/1; 1742/2; 1377/1; 1847/1; 1906/1; 1976/1; 2001/2; 2036/2 **Superfamily complement factor H repeat homology duplication; glycoprotein; transmembrane protein
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1828-1849,'D',1851-1875,'I',1877-2039 ##label RES
##cross-references GB:L17418; NID:g306678; PID:g306680
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Human C3b/C4b receptor (CR1). Demonstration of long homologous repeating domains that are composed of consensus repeats characteristic of C3/C4 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wong, W.W.; Klickstein, L.B.; Smith, J.A.; Weis, J.H.; Fearon, D.T.

Fearon, D.T.

Proc. Natl. Acad. Sci. U.S.A. (1985) 82:7711-7715

Identification of a partial cDNA clone for the human receptor for complement fragments C3b/C4b.
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J. Immunol. (1993) 151:6214-6224
Structure of the gene for the F allele of complement receptor type 1 and sequence of the coding region unique to the S
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##molecule_type DNA
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Similarity 31.4%;
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J. Immunol. (1993) 151:6214-6224
Structure of the gene for the F allele of complement receptor type 1 and sequence of the coding region unique to the S allele.
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complement C3b/C4b receptor (allotype S) precursor - human
complement receptor type 1 (CR1); surface glycoprotein CD35
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                          L.B.; Fearon, D.T.

J. Exp. Med. (1989) 169:847-863

Structure of the human CR1 gene. Molecular basis of the structural and quantitative polymorphisms and identification of a new CR1-like allele.
                                                                                                                                                                 Wong, W.W.; Cahill, J.M.; Rosen, M.D.; F. Bonaccio, E.T.; Morris, M.J.; Wilson,
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Pred. No. 1.18e-70;
66; Mismatches 110
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Wilson, J.G.; Klickstein,
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##cross-references EMBL:X14362; NI
##experimental_source clone CR1-4
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y Match 16.1%;
Local Similarity 31.4%;
hes 97; Conservative
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Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit and prediction of a secreted form of complement receptor type 1.
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    146 PDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD--GFWSKEKPKCVEISCKSPDVINGS
                                         155 EEF-FTYRSSVTYKCDPDFTLLGNASITCTVVNKTVGVWSPSPPTCERIICPWPKVLHGT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references EMBL: Z50051; NID: g899379; PIDN: CAA90391.1;
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                                                                                                                           98 SQIEFSCSEGYILIGSSTSYCEIQGKGVSWSDPLPECVIAKCGMPPDIS-NGK--HNGRE 154
                                                                                   90 VKAVYTCNEGYQLLGE-INYRECDTDG--WTNDIPICEVVKC-LPVTAPENGKIVSSAME 145
                                                                                                                                                                       32 YKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYG
                                                                                                                                                                                                             43 YNCRPGYSRASSSQSLYCKPLGKW-QIN-IA-CVKKSCRNPGDLQNGKVEVKT-D-FLFG 97
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ilarity 29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillarp, A.; Thern, A.; Dahlback, B. submitted to the EMBL Data Library, July 1995 Molecular cloning of rat C4b-binding protein alpha- and beta-chains: structural and functional relationships
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#formal_name Rattus norvegicus #common_name Norway rat
13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
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*title Primary sequence of an alternatively spliced form of CR1.

Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee erythrocytes.

**cross-references MUID:94292799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-661 ##label RES
##cross-references GB:L24921; NID:g557726; PID:g557727
[FICATION #superfamily complement factor H repeat homology
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                                                                                                                                                                                                                                                                152 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 208
   300 PRCTLKPCD 308
                                       326 PTCEVKSCD 334
                                                                       245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA- 299
                                                                                                                                                                                    209 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPPRVKCQALNKWEPELPSC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 15.9%;
Local Similarity 31.1%;
nes 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                38 FPIGTYLNYECRPGYYGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPD-PVNGMYHVI 93
                                                                                                                                                                                                                                                                                                   83 GNVFEYGVKAVYTCNEGYOLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                             24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y--SP-LRIKH--RTGDEITYQCRNGFYPATRGN-TAKC-TSTGWIPAPRCTLKPCDYPD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LITSPRPRKEDVYPVGTVLRYICRPGYEPATRQPMTVICQKDLSWSMLRGCKEICCPVPD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRPLPSCEEKSC-DNPYIPNGD 258
                                                                                                             S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASLRCTPQGDWSPAT 325
                                                                                                                                                                                                                                                                                                                                           KDI-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 151
                                                                                                                                                    EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement receptor 1 - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #length 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain complement factor H repeat
#domain complement factor H repeat
#domain complement factor H repeat
th 661 #checksum 8370
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#domain complement factor H repeat homology
#domain complement factor H repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #type fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
66; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 403; DB 2;
Pred. No. 3.49e-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 111; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 661;
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FH07\
FH08
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FH02/
FH03/
FH04/
FH05/
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DATE
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120-176
181-240
245-299
303-355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #cross-references MUID:88024997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381,428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                               117 KKHCRNPGYLDNG-Y-VNGETI-TFGSQIEFSCQEGFILVGSST-SSCEVRGKGVAWSNP 172
345 FSKWKGTAPQCKA-LCQKPEVGNGTLSDEK 373
                                               235 ESG-WRPLPSCEEKSCD-NPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCT 292
                                                                                         289 GNGNWSSLPTCEF-DCDLPPAIVNGYYTSM-VYSKIT-LVTYECDKGYRLVGKAIIS-CS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 PPPAIPNALPASDVNRTDFESHTTLKYECLPGYGRGISRMMVYCKPSGEW-EIS-VS-CA 116
                                                                                                                                                                                                                                                                                                                                  64 KRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTND 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 15.8%;
Local Similarity 27.9%;
es 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4BP controls the classical pathway of complement activation. It binds as a cofactor to C3b/C4b inactivation (C3bINA), which then hydrolytes the complement fragment C4b. It also accelerates the degradation of the C4bC2a complex (C3 convertase) by dissociating the complement fragment C2a.
                                                                                                                                                                                                                                   IPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD 177
                                                                                                                                                                                                                                                                                                                                                                                                                              PPRRNTEILTGSWSDQT-YPEGTQAIYKCRPGY-RSLGNVIMVCR-KGEWVALNPLRKCQ 63
                                                                                                                                         GF--WSKEKPKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCT 234
                                                                                                                                                                                      TYPYWSSSPPTCEKIICSQPNILHGYIVSGYKATYTHRDSVRLACLNGTVLRGRHVIECQ
                                                                                                                                                                                                                                                                                     FPECVIVKCGPPPDISNGK-HSGT-E-DF-YPYNHGISYTCDPGFRLVGSPFIGCTVVNK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In mouse, C4BP is a multimeric protein of noncovalently associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4b-binding protein alpha chain precursor - mouse C4BP; proline-rich protein #formal_name Mus musculus #common_name house mouse 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry (1987) 26:4668-4674 cDNA structure of murine C4b-binding protein, a regulatory component of the serum complement system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A27117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute phase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *superfamily C4b-binding protein alpha chain; complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kristensen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #length 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycoprotein; plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor H repeat homology
ute phase; chylomicron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the authors translated the codon GCT for residue 25 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH5\
#domain complement factor H repeat homology #label FH5\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *product C4b-binding protein alpha chain *status predicted *label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-469 ##label KRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T.; Ogata, R.T.; Chung, L.P.; Reid, K.B.M.; Tack,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #molecular-weight 51523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 402; DB 1; Let pred. No. 6.13e-69; 74; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement pathway; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #checksum 5359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps 28;
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Oy 293 STGWI-PAPRCTLKPCDYPDIKHGGLYHEN 321

Search completed: Thu Jun 8 21:45:47 2000 Job time: 23 secs.

\* Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Thu Jun 8 21:46:04 2000; MasPar time 12.45 Seconds 804.485 Million cell updates/sec

MPsrch\_pp

Run on:

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-09-316-163-11 (1-329) from US09316163.pep 2539 1 EDCNELPPRRNTEILTGSWS.......PDIKHGGLYHENMRRPYFPV 329

Scoring table: PAM 150 Gap 11

Post-processing: Min.Mnum Match 0% Lifting first 45 summaries Searched: 83857 spqs; 30454973 residues

Database: wiss-prot38 1:swissprot

Mean 44.764; Variance 62.937; scale 0.711

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1 3 3 4 4 4 4 4 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1	Result No.
2539 11772 433 409 409 400 400 388 371 371 367 367 341 341 334 333 333 334 333 333 333 333	Score
100.0 169.8 15.9 15.9 15.9 14.8 14.8 14.3 13.4 13.4 13.2 13.2 13.2 13.2 13.2 13.2 13.2 13.2	Query Match
1231 1234 52039 558 469 869 6108 6108 6108 6108 6108 6108 6108 6108	Query Match Length
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CFAH_HUMAN CFAH_MOUSE CABP_HUWAN CAL HUMAN CAL HUMAN CAL HUMAN CAL HUMAN CAL HUMAN CAL HUMAN APOH_MOUSE CABP_MOUSE CABP_MOUSE CABP_MOUSE CABP_MOUSE CABP_BOVIN LEM3_MOUSE CABP_BOVIN LEM3_MOUSE APOH_BOVIN APOH_GAMPAN LEM2_HUMAN LEM3_HUMAN LEM3_	ID
COMPLEMENT FACTOR H PR COMPLEMENT FACTOR H PR COMPLEMENT FACTOR H PR COMPLEMENT RECEPTOR TY C4B-BINDING PROTEIN AL C4B-BINDING PROTEIN PR C4B-BINDING PROTEIN PR COMPLEMENT CONTROL PRO P-SELECTIN PRECURSOR ( BETA-2-GLYCOPROTEIN I P-SELECTIN PRECURSOR ( COAGULATION FACTOR XII C4B-BINDING PROTEIN AL P-SELECTIN PRECURSOR ( COMPLEMENT CONTROL PRO COAGULATION FACTOR XII BETA-2-GLYCOPROTEIN I MEMBRANE COPACTOR PROT BETA-2-GLYCOPROTEIN I C-SELECTIN PRECURSOR ( C-	Description
0.00e+00 0.00e+00 1.94e-80 2.70e-80 2.70e-80 2.70e-70 2.38e-74 1.54e-60 3.54e-62 3.54e-62 3.54e-52 3.54e-59 1.54e-59 1.54e-59 1.54e-59 1.54e-59 1.54e-59 3.616-67 1.54e-59 3.72e-59 4.72e-59 4.72e-59 5.75e-54 6.68e-54 6.68e-54 7.71e-52 2.77e-52	Pred. No.

44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	
220	220	231	232	238	254	271	276	276	276	280	281	284	289	293	299	299	299	302	306	306	
8.7	8.7	9.1	9.1	9.4	10.0	10.7	10.9	10.9	10.9	11.0	11.1	11.2	11.4	11.5	11.8	11.8	11.8	11.9	12.1	12.1	
372	372	372	372	407	390	646	1019	485	297	507	331	340	1025	381	611	549	330	1033	769	551	
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LEM1_HUMAN	LEM1_PANTR	LEM1_MOUSE	LEM1_RAT	DAF2_MOUSE	DAF1_MOUSE	LEM3_BOVIN	LFC_TACTR	LEM2_BOVIN	APOH_RAT	DAF_CAVPO	CFHD_HUMAN	DAF_PONPY	CR2_MOUSE	DAF_HUMAN	LEM2_CANFA	LEM2_RAT	CFH1_HUMAN	CR2_HUMAN	LEM3_SHEEP	LEM2_RABIT	
L-SELECTIN			_			-	$\overline{}$	E-SELECTIN PRECURSOR	BETA-2-GLYCOPROTEIN	COMPLEMENT	_	-	_	_	E-SELECTIN	E-SELECTIN					
PRECURSOR (	PRECURSOR (	PRECURSOR (	PRECURSOR (	DECAY - ACCEL	DECAY - ACCEL	PRECURSOR (	TTING FACTO	PRECURSOR (	OPROTEIN I	DECAY - ACCEL	FACTOR H-LI	DECAY - ACCEL	RECEPTOR TY	DECAY - ACCEL	PRECURSOR (	PRECURSOR (	FACTOR H-LL	RECEPTOR TY	PRECURSOR (	PRECURSOR (	
1.15e-29	1 156-29	1 150-30	1.15e-32	J. DZC-34			6.U3E-44				2.98e-45	4.898-45	2.38e-47	2.11e-48	5.51e-50	5.51e-50	0.010.00	8.858-51	/./IE-52	7.71e-52	1

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EMBL; X04697; CAB41739.1; ALT_FRAME.

EMBL; M65294; AAA35948.1; -.

PIR; S00254; NBHUH.

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Complement alternate pathway; Plasma; Glycoprotein; Repeat; Sushi; Signal; 3D-structure; Polymorphism.
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-: SIMILARITY: CONTAINS 20 SUSHI (SCR) REPEATS.
-: CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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"Solution structure of the fifth repeat of factor H: a second e of the complement control protein module.";
Biochemistry 31:3626-3634(1992).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                   "Demonstration of an unusual allelic variation of mouse the complete cDNA sequence of the H.2 allotype.";
J. Immunol. 144:358-362(1990).
-i- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR TH THE TAIL
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POLYMORPHISM: TWO CODOMINANT ALLELES OF FACTOR H ARE PRESENT IN
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                                                                                                            Aso T., Okamura S., Matsuguchi T., "Genomic organization of the alpha protein gene.";
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01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
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Dahlback B. Smith C.A., Mueller-Eberhard H.J.;

"Visualization of human C4b-binding protein and its complexes with

ty vitamin K-dependent protein S and complement protein C4b.";

Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).

C. -! FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT

C. CISTIANION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

(CISTIANION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

(CISTIANION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

(CISTIANION ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3

CONVERTASE) BY DISSOCIATION OF THE C4BC2A COMPLEX (C3

CONVERTASE) BY DISSOCIATION THE COMPLEXOF FRAGMENT C2A. ALPHA

CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S

CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S

C. -!- SUBUNIT: DISULTIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS

CO S BOSSIBLE SORTS: A 570 KD COMPLEX OF TALPHA CHAINS AND 1 BETA

CHAIN, A 530 KD HOMOHEPTAMER OF ALPHA CHAINS OR A 500 KD COMPLEX

CO OF 6 ALPHA CHAINS AND 1 BETA CHAINS OR A 500 KD COMPLEX

CO OF 6 ALPHA CHAINS AND 1 BETA CHAIN THE CENTRAL BODY OF THE

CONTROL OF THE CHAINS AND 1 BETA CHAINS OR A 500 KD COMPLEX

CO OF 6 ALPHA CHAINS AND 1 BETA CHAINS OR A 500 KD COMPLEX

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                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                              EMBL;
                                                                                                                                    EMBL;
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                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chung L.P., Gagnon J., Reid K.B.M.; "Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and alignment of the fragments produced by limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE, AND LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteolysis with chymotrypsin and the peptides bromide treatment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 85296001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chung L.P., Bentley D.R., Reid K.B.M.;
"Molecular cloning and characterization of the cDNA coding binding protein, a regulatory protein of the classical path human complement system.";
biochem. J. 230:133-141(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Derivation of the sequence of the signal peptide in human C4b-binding protein and interspecies cross-hybridisation of the C4bp CDNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 49-88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Studies on the structure of the human C4b-binding protein gene."; FEBS Lett. 204:77-81(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 80-597 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF 6 ALPHA CHALNS AND I BELT COMMENTACLES, EACH WITH THE BINDING ALPHA CHAIN HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE BINDING SITE FOR C4B AT THE END.

SITE FOR C4B AT THE END.

SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.

SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.

SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.

CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
              M62480;
M62481;
M62482;
M62484;
M62484;
M62484;
                                                                                                                                                                                                     M31452;
M62486;
M62475;
M62476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunol. 22:427-435(1985).
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AAA36506.1;
AAA36506.1;
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AAA36506.1;
AAA36506.1;
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AAA36506.
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Matches 9
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PFAM; PF00084; sushi;
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                                                                       VEIKT-DL-SFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPPDI
QGCEALCCPEPKLNNGEITQHRKSRP
                  SCDN-PYIPNG--D-YS-PLRIK-HRTGDEITYQCRNGFYPATRGNTA-KC-TSTGWIPA
                                                                                                                       RNGR--HSG-E-ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKI
                                                                                                                                             FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYR-EC-DTD-GWTNDIPICEVVKCLPVTAP
                                                                                                                                                                                    SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT
                                                            SCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSCEEK
                                                                                                     ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS-D-D-
                                      SCINLPDIPHASWETYPRPTKEDVYVVGTVLRYRCHPGYKPTTDEPTTVICQKNLRWTPY 357
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97; Conse
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llarity 29.8%;
Conservative
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SUSHI 2.
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BY SIMILARITY.
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Pred. No. 1.94e-86;
68; Mismatches 132
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                                                                                                                                                                                                                                                                                        /FTId=VAR_001977.
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67E03F2EA85A16DD CRC64;
 383
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                                                                                                                                                                                                                            132;
                                                                                                                                                                                                                                                                                                                                                    BETA CHAIN) (POTENTIAL).
BETA CHAIN) (POTENTIAL).
                                                                                                                                                                                                                                                Length 597;
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THE SUPPLY OF THE PROPERTY OF 
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EMBL; M11617; AAA52298.1;
EMBL; M11618; AAA52299.1;
EMBL; Y00816; CAA68755.1;
EMBL; X05309; CAA28933.1;
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P17927;
01-NOV-1990
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01-NOV-1990 (Rel.
01-NOV-1997 (Rel.
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"Identification of distinct C3b and C4b recognition sites i human C3b/C4b receptor (CRI, CD35) by deletion mutagenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human C3b/C4b receptor (CR1). Demonstration of long homologous repeating domains that are composed of the short consensus repeats characteristics of C3/C4 binding proteins.";
J. Exp. Med. 165:1095-1112(1987).
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Fearon D.T.;
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MISCELLANEOUS: THIS IS THE SEQUENCE OF THE F SIMILARITY: CONTAINS 30 SUSHI (SCR) REPEARS.
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POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTI
POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTI
MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A
LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SCRS OF LHR-A
CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL
TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
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A24748; A24748; B24748; B24748; B24748; C24748; C24748; S03843; S03843

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PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

7 X SUSHI (SCR) REPEATS, LONG HOMOLOGOUS
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      Y SIMILARITY.
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Similarity 31.4%;
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66; Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of rat C4b binding protein alpha-
structural and functional relationships among human,
mouse, and rat proteins.";
J. Immunol. 158:1315-1323(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                     EMBL; Z50051; CAA90391.1; -. HSSP; P10998; 1VVC.
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15-JUL-1998
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                                                                                                                                                                                                           PFAM; PF00084; sushi; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97166082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                                                                                                                                                                             FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S SUBUNIT: DISSUFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS. SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 350
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                                                                                                                                                                                              pathway;
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(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
PROTEIN ALPHA CHAIN PRECURSOR.
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Rattus.
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bovine, rabbit,
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Best Local
Kristensen T., Ogata R.T., Chung L.P., Reid K.B.M., Tack B.F.;

"CDNA structure of murine C4b-bin," in protein, a regulatory con
of the serum complement system.";

Biochemistry 26:4668-4674(1987).

-!- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
-RUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
-RUNCTION: C1T BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR
(C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4I
ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3
                                                                                                                                                                                               C4BP_MOUSE STANDARD; PRT; 469 AA. P08607; 01-AUG-1988 (Rel. 08, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) C4B-BINDING PROTEIN PRECURSOR (C4BP).
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CARBOHYD
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Mus musculus (Mouse).

Fiikarvota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                       C4BPA OR C4BP
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Pred. No. 2.09e-78;
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                               OF COMPLEMENT INACTIVATOR
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SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.

SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.

CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. They by non-profit institutions as long a lifted and this statement is not removed.
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GNGNWSSLPTCEF-DCDLPPAIVNGYYTSM-VYSKIT-LVTYECDKGYRLVGKAIIS-CS
                                      GF--WSKEKPKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCT
                                                                            TVPVWSSSPPTCEKIICSQPNILHGVIVSGYKATYTHRDSVRLACLNGTVLRGRHVIECQ
                                                                                                                    IPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--DD 177
                                                                                                                                                            FPECVIVKCGPPPDISNGK-HSGT-E-DF-YPYNHGISYTCDPGFRLVGSPFIGCTVVNK 228
                                                                                                                                                                                                                                                                              PPRRNTEILTGSWSDQT-YPEGTQAIYKCRPGY-RSLGNVIMVCR-KGEWVALNPLRKCQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:88229; C4BP.
; PF00084; sushi; 6.
                                                                                                                                                                                                    KRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT-D-G--WTND 119
                                                                                                                                                                                                                                          KKHCRNPGYLDNG-Y-VNGETI-TFGSQIEFSCQEGFILVGSST-SSCEVRGKGVAWSNP 172
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A27117; NBMSC4.
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92; Conser
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27.9%;
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6 X SUSHI (SCR) REPEATS.
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SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 5.
SUSHI 6.
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 COMPLEMENT ACTIVATION 7, 5

J. MOI. BIOI. 272:253-265(1997).

-: FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

-: SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (BCA).

-!- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                              "Vaccinia virus complement-control protein prevents antibody-dependent complement-enhanced neutralization and contributes to virulence.";
                                                                                                                                                                                                                                                                                                                                                                                     Paoletti E.;
"The complete DNA sequence of Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kotwal G.J., Moss B.;
"Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCP_VACCV
P10998;
                                                                                                                                    Barlow P.N
                                                                                                                                                                                                                                                        FUNCTION.
---*TNE; 92115714.
                                                                                                                                                                                                                                                                                                                                Goebel S.J., Johnson G.P., Perkus
                                                                                                                                                                                                                                                                                                                                                 STRAIN-COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kotwal G.J., Moss B.; "Analysis of a large cluster of nonessential genes deleted from vaccinia virus terminal transposition mutant."; virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN
                                                                                                               "NMR studies of a viral protein that mimics the regulators
                                                                                                                                            Wiles A.P., Shaw G., Bright J.,
                                                                                                                                                                       STRUCTURE BY NMR OF 146-263
                                                                                                                                                                                                                                                      Isaacs S.N.,
                                                                                                                                                                                                                                                                                                        Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                             COMPLETE GENOME
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                                                                                                                                                                                                 Natl. Acad. Sci. U.S.A. 89:628-632(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                         S.J., Johnson G.P., Perkus M.E., Davis S.W.,
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adhesion and inflammation."; Cell 56:1033-1044(1989).

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PDB; 1VVD; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
PFAM; PF00084; sushi; 4.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 89168432.
Johnston G.I., Cook R.G., McEver R.P.;
"Cloning of GMP-140, a granule membrane protein of platelets and "Cloning of GMP-140, a granule membrane proteins involved in cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                      OI-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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                                                                                                                                                                                                           LEM3_HUMAN P16109;
                                                                                                     Eukaryota; Metazoa;
                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                           194
                                                                                                                                                                                                                                                                                                    208
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A31005; WMVZSP.
                                                                                                                                                                                                                                                                        SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                   SDQTYPEGTQAIYKCRPGYRS--LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                              OR GMRP.
                                                                                                                                                                                                                                                                                                  HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC
                                                                                                                                                                                                                                                                                                                              PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK
                                                                                                                                                                                                                                                                                                                                                                                 FTLTGGNVFEYGVKAVYTCNEGYQLLGEIN-YRE-CDTDG--WINDIPICEVVKCLPVTA 133
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34.2%;
                                                                                        Catarrhini;
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                                                                                                      Chordata; Craniata; Vertebrata; Mammalia;
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Pred. No. 5.28e-74;
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SUSHI 2.
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                                                                                          Hominidae;
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Ruidavets J.B., Arveiler D., Luc G., Cambien F.;

"The P-selectin gene is highly polymorphic: reduced frequency of the pro715 allele carriers in patients with myocardial infarction.";

Hum. Mol. Genet. 7:1277-1284(1998).

-i- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS FOR CARBOHYDRATES ON NEUTROPHILS AND MONOCITES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIAVIL-LEWIS X.

-i- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS.

ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO

commercial

on 8

Bajorath J., Stenkamp R., Aruffo A.; "Knowledge-based model building of proteins: concepts and examples."; Protein Sci. 2:1798-1810(1993).

Herrmann S.M., Ricard S.,

Nicaud V.,

Mallet C., Evans

Α.,

98334547

VARIANTS ASN-331; ASP-603; VAL-640 AND PRO-756.

MEDLINE;

Biochemistry 35:13733-13744(1996).

3D-STRUCTURE MODELING OF 42-161

MEDLINE;

94093388

Furie B.;

MEDLINE;

STRUCTURE BY NMR OF 160-199

97057176

Freedman S.J., Sanford D.G., Bachovchin W.W., Furie B.C.,

Baleja J.D.,

"Structure and function of the epidermal growth factor domain of P-

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SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 9 SUSHI (SCR) REPEATS.

DATABASE: NAME=PROW; NOTE=CD guide CD62P entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
                                             173610
                                                                       A30359; A30359
                                                     1KJD; 03-APR-96.
                                                             1FSB; 01-APR-97.
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M60217; AAA35910.1;
                                   PR00343; SELECTIN
PS00022; EGF_1; 1.
PS01186; EGF_2; 1.
PS00615; C_TYPE_LECTIN_1;
PS50041; C_TYPE_LECTIN_2;
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; PF00059; lectin_c; 1.
; PF00084; sushi; 9.
adhesion; Transmembrane;
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                                                          830 AA;
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     Conservative
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                Score 376; DB 1;
Pred. No. 1.02e-70;
                                                                                             /FTId=VAR_004194.
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at; Polymorphism; 3D-structure.
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EMBL; D10056; BAA00945.1; -. EMBL; S70439; AAB30789.1; -. EMBL; Y11356; CAA72190.1; -.
                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 92372000.

Monaka M., Matsuda Y., Shiro

Molecular cloning of mouse

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Q1-APR-1993 (Rel. 25, Created)
O1-APR-1993 (Rel. 25, Last sequence update)
O1-APR-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) (B2GPI).
APOH OR B2GPI.
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STRAIN=BALB/C; TISSUE=LIVER;
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Riochem. Biophys. Res. Commun. 200:1521-1528(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whitehead A.S.;
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SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
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2-glycoprotein I and mapping of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heparin-binding;
SIGNAL 1
CHAIN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MG
                                                                                                                                                      LEM3_RAT STANDARD; PRT; 768 AA.

P98106;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUE-1999 (Rel. 38, Last annotation update)
15-JUE-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
CCD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
           MEDLINE; 94333817.
Auchampach J.A., O
                                                                                                          Eukaryota;
                                                                                           Eutheria; Rodentia;
                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                    199
Auchampach J.A., Oliver M.G., Ande
"Cloning, sequence comparison and
                                              TISSUE-LUNG
                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPEGTQAIYKCRPGYRSLGNVIM-VCR-KGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
                                                                                                                                                                                                                                                                                                                        PNGD-YSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                    KATVLYQGMRVK 281
                                                                                                                                                                                                                                                                                                                                                                                                    NGYVNYPAKPVLLYKDKATFG--CHETYKLDGPEEAECTKTGTWSFLPTCRE-SCKLPVK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDYRPSAGNNSLYQDTVVFKCLPHFAMIGNDTVMCTEQGNWTRL-PECLEVKCPFPPRPE 212
                                                                                                                                                                                                                                                                                                                                                                                  NG--S-PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSCDNPYI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK-SPDVI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I:88058; APOH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 74; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1VVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.6%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38619
                                                                                               Sciurognathi;
                                                                                                              Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA-2-GLYCOPROTEIN I.
4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
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Pred.
49; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MODIFIED-SUSHI.
BY SIMILARITY.
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G -> R (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
      Anderson D.C., Manning A.M.;
and in vivo expression of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasma; Repeat; Sushi; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> R (IN REF. 2).
C83F8A6EBD51C940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 110; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371;
No. :
                                                                                                  Muridae;
   in vivo expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L; DB 1;
2.38e-69;
                                                                                                               Vertebrata;
                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 345;
                                                                                                  Mammalia;
Rattus.
     the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
        RT encoding rat P-selectin.";

11. Gene 145:251-255(1994).

12. Gene 145:251-255(1994).

12. CI FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS

12. CI CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE

13. INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH

14. CI CI CHARLAR LOCATION: TYPE I MEMBRANE PROTEIN.

15. CI SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

16. CI TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,

17. CI CI INDUCTION: ACUTE INFLAMATION (PROBABLY).

18. CI INDUCTION: ACUTE INFLAMATION (PROBABLY).

19. SIMILARITY: CONTAINS 1 COTYPE LECTIN FAMILY DOMAIN.

19. CI SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

19. CI SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L23088; AAA60325.1; -.
HSSP; P16109; IFSB.
PRINTS; PR00343; SELECTIN.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01615; C_TYPE_LECTIN_1; 1
PROSITE; PS00641; C_TYPE_LECTIN_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal;
          Transmembrane;
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BY SIMILARITY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENT IAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; EGF-like domain; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUSHI (SCR) REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                               "Molecular cloning of the b subunit of mouse coagulation factor XIII and assignment of themsene to chromosome 1: close evolutionary relationship to complement factor H.";

Genomics 15:335-42(1993).

-i- FUNCTION: THE B CHAIN OF FACTOR XIII IS NOT CATALLYTICALLY ACTIVE, BUT IS THOUGHT TO STABILIZE THE A SUBUNITS AND REGULATE THE RATE OF TRANSGLUTAMINASE FORMATION BY THROWBIN.

-i- SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS.
-i- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER AND KIDNEY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
COAGULATION FACTOR XIII B CHAIN PRECURSOR (EC 2.3.2.13) (PROTEIN-
GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE B CHAIN) (TRANSGLUTAMINASE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-B10.D2/OSN; TISSUE-LIVER; MEDLINE; 93224141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F13B_MOUSE STANDARD;
Q07968;
Q1-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               Natsuume-Sakai S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nonaka M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 80; Conse
                                                                                                                                                                   SIMILARITY: CONTAINS 10 SUSHI (SCR) REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPLKYQSACSFSCDEGSLLVGASVIRCLATGHWSEAPPECQAVSCTPLLSPENGTMTCIQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLRIKHRIGDEITYOCRNGF-YPATRGNTAKCTSTG-W-IPAPRC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHVHGEFSVGSTCHFSCNEEFELLGSR-NVE-CTVSGRWSAPPPTC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIIYKENERF-QYKCNMGYEYSERGDAVCTESG-WRPLPS-CEEKSCDNPYIPN-G--DY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLGHSNYKSTCQFMCDEGFYLSGPERLDCSPSGHWTGSPPMCEAIKCPEIFAPEQGSLDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REYHFGQAVRFYCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP-DVINGSPIS-Q
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Pred. No. 2.94e-68
53; Mismatches 13
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26FD7E8a5F3F1316 CRC64;
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PIR; A46013; A46013.
HSSP; P10998; IVVC.
MGD; MGI:88379; F13B.
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                       YHENMRRPY 326
                                                                NNIQLKWKY 472
                                                                                                                                                                                      PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSC-EE-KSCDNP-YIPNGD
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                                                                                                   Y-SPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGL
                                                                                                                                          VYDGLLASYTTGSSVEYRC-NEYYLLKGSETSRCEQGAWSSPPVC-LEPCTI-DVDHMNR
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Pred. No. 3.61e-67;
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"Bowine C4b binding protein. Molecular cloning of the alpha- ar
beta-chains provides structural background for lack of complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C4BPA.
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Immunol. 153:4190-4199(1994).

TEUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DESCRIPTION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DESCRIPTION THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.
                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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(Rel. 35
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8 x SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 5.
SUSHI 7.
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Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-APR-1999 (Rel. 38, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LECKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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                                                                                                                                                                                                                                            Blood 80:795-800(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weller A., Isenmann S., Vestweber D.;
"Cloning of the mouse endothelial selectins. E
and P-selectin is inducible by tumor necrosis
J. Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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"Molecular cloning and analysis
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                                               FUNCTION: CA(2+) DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS TO CARROHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WELLBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
     INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS00611; C_TYPE_LECTIN_2;
DENM: BENNONDE FGF. 1
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PFAM; PF00059;
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
THE HUMAN SUSHI-2 EQUIVALENT.
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adhesion;
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ENDOCYTOSIS SIGNAL (PROBABLE).
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation updat
COMPLEMENT CONTROL PROTEIN HOMOLOG PRECURSC
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92260674.
Albrecht J.-C., Fleckenstein B.;
New member of the multigene family of complement control herpesvirus saimiri.";
J. Virol. 66:3937-3940(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B., Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B., Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
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Viruses; dsDNA viruses, no I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure of the herpesvirus saimiri genome."; Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 PLRIKHRTG-DEI-TYQCRNGFYPATRGNTAKCTSTG-w-IPAPRC
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nes 77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND A SECRETED ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).
SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSHVHGEFGVGSICHFSCNEDFELLGSENVE-CTVSGRWSAPPPTC 567
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llarity 26.9%;
Conservative
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Pred. No. 9.54e+62;
52; Mismatches 134
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EMBL;

B42534; WMBE2E A42534; WMBE1E

EMBL;

X64346; CAA45626.1; -. X64346; CAA45627.1; -. X60283; CAA42823.1; -. X60283; CAA42822.1; -.

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HSSP; P10998; 1VVC.
PFAM; PF00084; sushi; 4
Signal; Repeat; Sushi;
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SIGNAL
CHAIN
                                                                                                                                                                                                                                P05160;
13-AUG-1987
01-AUG-1990
15-JUL-1999
COAGULATION
GLUTAMINE GA
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SEQUENCE
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CARBOHYD
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SEQUENCE OF 2-661
MEDLINE; 87026535.
                                                                                                                                                                                                                   CHAIN).
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                                              Biochemistry
                                                                                             Bottenus
                                                                                                         MEDLINE;
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                         Eutheria;
                                                                                                                                                                        Eukaryota;
                                                                             "Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                           196
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                                                                                                                                                                                     sapiens (Human)
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Similarity 31.9%;
74; Conservation
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                                                                        91105054.

R.E., Ichino:

Lide sequence
                                                                                                                                                                                                                                87 (Rel. 05, Created)
90 (Rel. 15, Last sequence update)
99 (Rel. 38, Last annotation update)
ON FACTOR XIII B CHAIN PRECURSOR (EC
GAMMA-GLUTAMYLTRANSFERASE B CHAIN)
                                                                                                                                                         Primates;
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360
                                                                                                                                                                        Metazoa;
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                                                29:11195-11209(1990).
                                                                           , Ichinose
equence of
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                                                                                                                                                                                                                                                                                                                              STANDARD;
                   FROM
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                                                                                                                                                       Catarrhini;
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                   N.A
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the
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Pred.
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SHORT ISOFORM)
MISSING (IN SHO)
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gene f
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COMPLEMENT CONTROL PROTE
3 X SUSHI (SCR) REPEATS.
SUSHI 1.
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                                                                                                                                                                        Craniata;
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                                                                                                                                                         Hominidae;
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No. 3
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                                                                                the
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                                                                                                                                                                        Vertebrata;
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                                                                               subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 360;
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                                                                                of.
                                                                                                                                                                         Mammalia;
                                                                                human
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rcninose A., McMullen B.A., Fujikawa K.,
"Amino acid sequence of the b subunit of
composed of ten repetitive segments.";
Biochemistry 25:4633-4638(1986).
[3]
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"Two genetic defects in a patient with complete deficiency of the b-
subunit for coagulation factor XIII.";
Blood 82:145-150(1993).

-i- FUNCTION: THE B CHAIN OF FACTOR XIII IS NOT CATALYTICALLY ACTIVE,
BUT IS THOUGHT TO STABILIZE THE A SUBUNITS AND REGULATE THE RATE
OF TRANSGLUTAMINASE FORMATION BY THROMBIN.

-i- SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS.

-i- SUBUNIT: TETRAMER OF TWO A CHAINS AND HABITUAL ABORTION.

-I- SIMILARITY: CONTAINS 10 SUBHI (SCR) REPEATS.
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between
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EMBL; M14057; AAA88042.1; -.

EMBL; X51823; CAA36123.1; -.

PIR; A23830; A23830.

PIR; A36397; A36397.

PIR; A36397; A36397.

PIR; S09980; S09980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
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10 x SUSHI (SCR) REPEATS.
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Y SIMILARITY.
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of human factor
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                                              317 LYHENMRRPY 326
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                                                                                        259 YSP-LRIKHRTGDEITYQCRNGFYPATRGNT-AKCTSTGWIPAPRCTLKPCDYPDIKHGG 316
                                                                                                            407 VADGILASYATGSSVEYRC-NEYY-LLRGSKISRCEQGKWSSPPVC-LEPCT-VNVDYMN 462
                                                                                                                                     202 PISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSC-EEK-SCDNP-YIPNGD 258
                                                                                                                                                           347 ANLHSKIYYNGDKVTYACKSGYLLHGSNEITCNRGKWTLPPECVENNENCKHPPVVMNGA 406
                                                                                                                                                                                 147 DREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVE----ISCKSPDVI-NGS 201
                                                                                                                                                                                                                                                                                            178 YECATGYYTAGGKKTEEVECLTYGW-SLTP--KCTKLKCSSLRLIENGYFH-PVKQTYEE 233
                                                                                                                                                                                                292 YR--H-GEIVHIECELNFEIHGSAEIRC-EDGKWT-EPPKCIEGQEKVACEEPPFIENGA 346
                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                             32 YKCRPGY-RSLGN-VIMV-CRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEY 88
                                                                                                                                                                                                                                 GVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEV--VKCLPVTAPENGKIVSSAMEP 146
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57; Mismatches 134; Indels 30;
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Run on: MPsrch\_pp Description: Perfect Score: Tabular output not generated. Statistics: Database: Post-processing: Scoring table: Sequence: Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Gap 1 Minimum Match Listing first Thu Jun 8 21:46:38 2000; 22**,**8878 seqs, PAM 150 1 EDCNELPPRRNTEILTGSWS......PDIKHGGLYHENMRRPYFPV 329 sptrembl12 Mean 43.988; Variance 63.846; scale 0.689 1:sp\_archéa 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_4rvertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus θ9334122 residues 45 summaries MasPar time 30.28 Seconds 753.376 Million cell updates/sec

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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21	372	14.7	315	σ	Q28770		.96e-6
22	373	14.7	679	11	Q99254	COMPLEMENT RECEPTOR TY	1.06e-67
23	373	14.7	740	4	095508		1.06e-67
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26	360	14.2	808	11	Q61408	COMPLEMENT FACTOR H-RE	2.93e-64
27	357		263	14	Q07033		.81e-
28	357	14.1	263	14	Q89859	HOMOLOG OF VACCINIA VI	1.81e-63
29	355	14.0	263	14	Q89076	B19L.	6.10e-63
30	354	13.9	754	σ	Q28290	CELL ADHESION MOLECULE	1.12e-62
31	350	13.8	263	14	Q89061	D15L.	1.26e-61
32	343	13.5	974	σı	P91658		8.72e-60
33	341	13.4	559	11	Q63135	COMPLEMENT REGULATORY	2.92e-59
34	338	13.3	349	4	Q15429		1.78e-58
3 5	336	13.2	497	11	Q63612	ש	5.94e-58
36	336	13.2	740	4	095507	.1.1 (SELE	5.94e-58
37	331	13.0	285	σ	019126	COFACTOR	1.20e-56
38	331	13.0	285	σ	019127		1.20e-56
ယ <b>9</b>	328	12.9	369	σ	P79138	MEMBRANE COFACTOR PROT	7.28e-56
40	328	12.9	1045	σ	046545	$^{\circ}$	7.28e-56
41	323	12.7	285	σ	019121		1.46e-54
42	318	12.5	377	6	062838		2.90e-53
43	317	12.5	378	6	062837	MEMBRANE COFACTOR PROT	5.27e-53
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45	316	12.4	1087	4	Q14212	EPSTEIN-BARR VIRUS COM	9.5/e-53

## ALIGNMENTS

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RESULT
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Q14570 PRELIMINARY; PRT; 449 AA.
Q14570; P78435;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                               Thesis (1993), Inmunologia, Hospital Trias I Pujol, Spain.
EMBL; X07523; CAA30403.1; --
EMBL; M12383; AAA52013.1; --
EMBL; U56979; AAB01987.1; --
EMBL; Z29665; CAA82763.1; --
EMBL; R29665; CAA82763.1; --
EMBL; P10998; 1VVC.
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MEDLINE; 88134059.
RIPOCHE J., DAY A.J., HARRIS T.J.R., SIM R.B.;
"The complete amino acid sequence of human complement factor H.";
Biochem. J. 249:593-602(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRISTENSEN T., WETSEL R.A., TACK B.F.; "Structural analysis of human complement protein H: homology with C4b binding protein, beta 2-91/coprotein I, and the Ba fragment of B2."; J. Immunol. 136:3407-3411(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-9 FROM N.A. DOMINGUEZ O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-19 FROM N.A. VIK D.P., WILLIAMS S.A.;
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                                                                 SEQUENCE
                                                                                                                                              SIGNAL
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                                                                         449 AA;
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   100.0%; Score 2539; DB 4;
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51033 MW; 61231E1B CRC32;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X98697; CAA67257.1; -. HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 SOAMES C.J., DAY A.J., SIM R.B.;
"Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b.";
Biochem. J. 315:523-531(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae; Bos.
260 SPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGLYH
                           187 RPELSKYRGOOKITYECKKGFFPEIRGTDATCTRDGWVPVPRCAWKPCSYPVIKHGRLYY 246
                                                                                                                            140 VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319
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                                                             GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDY
                                                                                             GQAVLPKATYKQNERVQYRCAAGFEYGQRGDTVCTKSGWTPAPTCIEITCDPPRIPNGVY
                                                                                                                                                FSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPPVILN 126
                                                                                                                                                                                            LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                                                                                                                              PF00084; sushi; 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCOKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                  153;
                                                                                                                                                                                                                                                                                h 48.7%;
Similarity 61.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96202005.
                                                                                                                                                                                                                                                                                                                                 669 AA;
                                                                                                                                                                                                                                                                                                                                                    669
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                          669
75683 MW; FAF0D174 CRC32;
                                                                                                                                                                                                                                                                              Score 1236; DB 6;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                               35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.00e+00; 0; Mismatches 0;
                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                             Length 669;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                             2;
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                                                                259
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Best Local
                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Futheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                    Q14006 PRELIMINARY; PRT; 657 AA.
Q14006;
Q1-NOV-1996 (TremBLrel. 01, Created)
O1-NOV-1996 (TremBLrel. 01, Last sequence update)
O1-NOV-1999 (TremBLrel. 12, Last annotation update)
MEDLINE; 88025472.

DAY A.J., RIPOCHE J., LYONS A., MCINTOSH B.,
"Sequence analysis of a cDNA clone encoding the human complement factor H.";
                                                                                                                                                                  ΗĦ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91275 PRELIMINARY; PRT; 1053 AA.
Q91275;
Q91275;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 02, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
Paralabrax nebulifer (barred sand bass).
                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                COMPLEMENT H FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L21703; AAA92556.1; --
HSSP; P08603; 1HFH.
PFAM; PF00084; sushi; 16.
                                                                                                                                                                                                                                                                                                                                           257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neblifer).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement_regulatory plasma protein from barred sand bass (Parablax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAHMEN A., KAIDOH T., ZIPFEL P.F., GIGLI I.; "Cloning and characterization of a cDNA representing a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94318039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perciformes; Percoidei; Serranidae; Paralabrax.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 AEGNDFYFGSKYYYTCQKGYQMYSRINYRRCYAEGWDGYVPYCESQQC-PLIHYDNNVQV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 23.7%; Score 603; DB 13; Local Similarity 34.1%; Pred. No. 1.99e-130; hes 101; Conservative 49; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 EASYPGGRQVRVGCNVGY-S-GFFKLVCVEGKWETRGA--KCQPRSCGHPGDAQFADFHL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 ENMRRPYFP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DQTYPEGTQAIYKCRPGYRSLGNVIMYCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 SY--RGYFP 253
                                                                                                                                                                                                                                                                                                                                  GDYSPL-RIKHRTGDEITYQC-RNGFYPATRGNT--AKCTSTG-WIPAPRCTLKPC 307
                                                                                                                                                                                                                                                                                                                                                                 TRYEPAYRNLFSPGETLKVICARTSWISTPQETSVVTTCQDNGEWSIRPTCQEVRC 334
                                                                                                                                                                                                                                                                                                                                                                                                    GSPISQKIIYKENERFQYKCNMGYEYSERGDA-V--CTESGWRPLPSCEEKSCDNPYIPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                      GNVPGAIREYKENDVLHYECDRAFKHIDRPSTCIKQGIKAEWSPTPLCESIKCRLTIMDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. 301:391-397(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1053 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49; Mismatches 129;
                    the C-terminal
                                   HARRIS T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1053;
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              SIM R.B.;
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FIRESULPT
OCCUPANT
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O9WRU2 PRELIMINARY; PKT; 040 AA.
O9WRU2:
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
COMPLEMENT BINDING PROTEIN.

update)

645

Macaca mulatta rhadinovirus 17577. Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.

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Best Local S
                                                                                                                      Matches
                                                                                                                                                 Query Match
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EMBL; M17517; AAA52016.1; -.
HSSP; P08603; 1HFH.
PFAM; PF00084; sushi: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENT FACTOR H-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TIEMBLIER). 01, Created)
01-NOV-1996 (TIEMBLIER). 01, Last sequence update)
01-NOV-1999 (TIEMBLIER). 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q61407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q61407
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 CSQ-PPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKW-S-SP-PQ 351
                                                                                                                                                                                                            EMBL; M29010; AAA37415.1; -. HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                        VIK D.P., MUNOZ-CANOVES P., KOZONO H., CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
                                                                                                                                                                                 PFAM; PF00084; sushi; 7
SEQUENCE 452 AA; 516
                                                                                                                                                                                                                                           Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                    VIK D.P.,
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
296 WIPAPRCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
                                                          236 SGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 18.7%;
Local Similarity 27.5%;
es 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CNELPPRRNTEILTGSWSDQ-TYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRK 61
                          75 WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPV 108
                                                                                       15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHRSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
                                                                                                              17.3%;
Local Similarity 56.4%;
es 53; Conservation
                                                                                                                                                                                                                                                                                                                    Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEGLPCKSPPEISHGVVAHMSDS-YQYGEEVTYKCFEGFGIDGPAIAK-CLGEKWSHP-P 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QWSEPPKC-LHPC 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEPPOCKDSTGKCGPPPPIDNGDITSFPLSYYAPASSYEYQCQN-LYQLEGNKRITCRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEKPKCVEISC-KSPDVINGSPIS-QKIIYKENERFQYKCNMGYE-YSERGDAVCTESGW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GRPTCRDTSCVNPPTVQNAYIVSRQMSKYPSGERVRYQCRSPYEMFGD-EEVMCLNGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCIKTDCLSLPSFENA-IPMGEKK-D-VYKAGEQVTYTCATYYKMDGASNVTCINSR-WT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWIPAPRCTLKPC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPLPSCEEKS - - CDNPY - IPNGDYSPLRIK - HRTGDEITYQCRNGFYPATRGNTAKCTST
                                                                                                                                                                                                                                                                                                                                                  MUNOZ-CANOVES P., KOZONO H., MARTIN L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657 AA; 74247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      0:0-0(0).
                                                                                                                                                                                  51602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 476; DB 4; Length 657; Pred. No. 1.99e-95; 72; Mismatches 132; Indels 23;
                                                                                                                         16;
                                                                                                                                   Score 438; DB 11;
Pred. No. 4.10e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F4AB5238 CRC32;
                                                                                                                                                                                  45C0BF61 CRC32;
                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 AA
                                                                                                                                                                                                                                                                            MARTIN L.G.,
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                                                                                                                                                    Length 452;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Mus.
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ΩV g

337 EKYSVGASVELICRPGFTKMQSTVSVECLSNGTWTAPNA--KCHRKKCPTPQELLNGEYI 394

395 VISGEDAFKYGINITYKCNEGYQLLGSMYRICMLKDDLKTVDMEPKAPICDIEKCKPPPQ 454

80 LTGG-NVFEYGVKAVYTCNEGYQLLGE-IN-Y--REC-DTDGWINDIPICEVVKCLPVTA 133

Query Match Best Local Matches

17.2%;
Local Similarity 30.9%;
nes 72; Conservet

Score 436; DB 14; I Pred. No. 1.42e-84; 50; Mismatches 94;

Length 645;

Indels 17;

Gaps

14;

60FB82D6 CRC32;

J. Virol. 73:3040-3053(1999). EMBL; AF083501; AAD21332.1; -. SEQUENCE 645 AA; 71526 MW;

herpesvirus 8."; J. Virol. 73:304

SEARLES R.P., MEDLINE; 99174001. SEQUENCE FROM N.A.

"Sequence and genomic analysis of a Rhesus macaque rhadinov similarity to Kaposi's sarcoma-associated herpesvirus/human

BERGQUAM E.P., AXTHELM M.K., WONG S.W.; genomic analysis of a Rhesus macaque rhadinovirus with

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510 APNIAHGKLLTGSSSYYKYGQSYTIGCETGFTLIGSEISTCKDSSWDPPLPTC 562

194 SPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESGW-RPLPSC

134 PENGKIVSSAMEDDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193

ITNGKY--HPVK-DF-YQYLDTVTFSCNRDFSLVGDEMTTCISNT-WNKPFPRCEQITCS 509

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Q61405 Q61405;

PRELIMINARY;

PRT;

303

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT FACTOR H-REDATED PROTEIN.

SEQUENCE FROM N.A. MEDLINE; 90153969.

VIK D.P., MUNOZ-CANOVES P., KOZONO H.,

MARTIN L.G.,

CHAPLIN D.D.

Eukaryota; Metazoa; Mus musculus (Mouse)

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Chordata; Craniata; Vertebrata;

Mammalia; Mus.

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                                                                          Query Match
Best Local S
                                                              Matches
236 SGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTG
                              15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHKSDDEIRYECNYGFYPVTGSTVSKCTPTG
                                                           17.1%;
Similarity 55.3%;
52; Conservation
                                                               Score 433; DB 11;
Pred. No. 9.20e-84;
17; Mismatches 25
                                                                                              Length 303;
                                                                   Indels
                                                                    0;
                                                                   Gaps
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"Identification and sequence analysis of four complement factor related transcripts in mouse liver.";
J. Biol. Chem. 265:3193-3201(1990).
EMBL; M29007; AAA37413.1;
HSSP; P10998; 1VC.
PFAM; PF00084; Sushi; 4.
SEQUENCE 303 AA; 34498 MW; 39350FD1 CRC32;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                            Proc. Natl. Acad, Sci. U.S.A. 93:14862-14867(1996).
                                                                                                                                                                                                                                                                                    Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                          P88903;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence of the control of the co
SEQUENCE FROM N.A
                                                                                             RUSSO J.J., BOHENZKY R.A., CHIEN M.C., CHEN J., YAN M., MADDALENA D., PARRY J.P., PERUZZI D., EDELMAN I.S., CHANG Y., MOORE P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8).";
                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 97121480.
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040912
040912;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seg-
01-AN-1999 (TrEMBLrel. 12, Last ann
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"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?";
J. Virol. 71:4187.4192(1997).
EMBL; U93872; AAB62602.1; -.
HSSP; P10998; IVVC.
FFAM; PF00084; sushi; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 PLRIKHRTGDEITYQCRNGFY-PATRGNTAKCTST 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Last annotation update)
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Pred. No. 1.10e-82;
59; Mismatches 110;
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Best Local :
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BIRNINGHAM D.J., LOGAR C.M., SHEN X.P., CHEN W.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; L77977; AAA99004.1;
HSSP; P08603; 1HFI.
PEAM; PF00084; sushi; 7.
NON_TER 1.
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O289769;
O289769;
O1-NOV-1996 (TIEMBLIEL. 01, Created)
O1-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
O1-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
COMPLEMENT RECEPTOR (FRAGNENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
120 IPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVREVCN--SGYK-I-E--GDEEM
                                                                163 TPICEIIPCGLPPTIA-NGDFISTSRE---YFPYGSVVTYRCNLGSGRKKLFELVGEPSI 218
                                                                                                                                                                                                105 TRKSCRNPKD-PVNGMVHVIKDI-QFGSQINYSCNKGYRLIGSSSATCIISGNTVIWDNE 162
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HSSP;
PFAM;
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Science 274:1739-1744(1996).
EMBL; U75698; AACS7082.1; -.
HSSP; P10998; IVVC.
                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                52 EQLPFARPIN-LIDA-SE--FPVGTYLKYECLPGYHGKPFSI-ICLKNSVWTSAKD--KC 104
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MOORE P.S., BASHOFF C., WEISS R.A., CHANG Y.;

"Molecular mimicry of human cytokine and cytokine response pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 PLRIKHRTGDEITYQCRNGFY-PATRGNTAKCTST 294
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                                                                                                                                                                                                                                                                   4 NELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKC 62
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                                                                                                                                                                                                                                                                                                                                                                                                       h 16.8%; Score 426; DB 6; Length 522; Similarity 32.1%; Pred. No. 7.11e-82; 111; Conservative 74; Mismatches 119; Indels 42;
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Similarity 29.8%; Pred. No. 2.05e-82;
82; Conservative 59; Mismatches 110
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
   Q29528
Q29528;
Q1-NOV-1996
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1391 FPVGTSLNYECRPGY--FGKMFSISCLENLVWSSVED--NCRKSCGPPPE-PFNGMVHI 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Immunol. 153:691-700(1994).
EMBL; L24920; AAA51438.1; -.
HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 9429799. 
BIRMINGHAM D.J., SHEN x.P., HOURCADE D., NICKELLS M.W., ATKINSON J.P. BIRMINGHAM D.J., SHEN x.P., HOURCADE D., NICKELLS M.W., ATKINSON J.P. "Prinary sequence of an alternatively spliced form of CR1. Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                         1679 PRCTVKSCDDFLGQLPHGRVLFPLNLQ 1705
                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                     245 EEKSCDNP-YIPNGDYSPLRIKH-RTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIP-A
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Local Similarity 29.1%;
hes 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRGAASLHCTPQGDWNPEAPICTVKSCDDFLGQLPHGRVLFPLNLQ 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STNKCTAPEVENAIRVPGNRSFFSLTEIVRFRCQPGFVMVGSHTVQCQTNGRWGPKLPHC 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYSNNRAS---FHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSPPPRCI 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGNVFEYGVKAVYTCNEGYQLLGE--INYRECDTD-GWINDIPICEVVKCLPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGTFTLT 81
                                                                                                                                                                                                                             PRCTLKPCD-Y-PDIKHG-GLYHENMR 323
                                                                                                                                                                                                                                                                                                                                                                                                              S-RVCQPPPEILHGEHTPSHQDNFSPGQEVFYSCEPG-Y-DLRGAASLHCTPQGDWSPEA 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIS-CKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
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2014 AA;
   (TrEMBLrel. 01, (TrEMBLrel. 01,
                                                                                                    PRELIMINARY;
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Pred. No. 4.57e-81;
74; Mismatches 119; Indels 3
      Created)
Last sequence update)
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                                                                                                           1911 AA
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Best Local Similarity 29.8%;
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SEQUENCE FROM N.A.

VIX D.P., WONG W.W.;

SLDmitted (JUN-1993) to the EMBL/G6

EMBL; L17418; AAB60694.1; --

EMBL; L17390; AAB60694.1; JOINED.

EMBL; L17391; AAB60694.1; JOINED.

EMBL; L17392; AAB60694.1; JOINED.

EMBL; L17393; AAB60694.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1303 FPVGTSLNYECHPGY--FGRMFSISCLENLVWSSVED--NCRRKSCGTPPE-PFNGMVHI 1357
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Last annotation update) COMPLEMENT RECEPTOR 1 (FRAGMENT).
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016745;

01-NOV-1996 (TrEMBLrel. 01,

01-NOV-1996 (TrEMBLrel. 01,

01-NOV-1999 (TrEMBLrel. 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1591 PICTVKSCD 1599
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 94065175. VIK D.P., WONG W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Ci
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENT RECEPTOR 1.
                                                                                                                                                                                                                                                               "Structure of the gene for the F allele of complement receptor type 1 and sequence of the coding region unique to the S allele.";
J. Immunol. 151:6214-6224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 EEKSCDNP-YIPNGDYSPLRI-KHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIP-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 YPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGTFTLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STNKCTAPEVKNGIRVPGNRSFFSLNEIVRFRCQPGFVMVGSHTVQCQTNNRWGPKLPHC 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYSNNR-TS--FHSGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGAWSSPPPRCI 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTDT-QFGSTVNYSCNEGFRLIGSPSTTCLVSGNNVTWDKEAPICEIISCKPPPTISNGD 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIS-CKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP-LPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                     to the EMBL/GenBank/DDBJ
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Pred. No. 4.14e-78;
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Last annotation update)
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Best Local
                                                     Q16744 PRELIMINARY; PRT; 2489 AA.
Q16744; Q16744;
Q1-NOV-1996 (TrembLrel. 01, Created)
Q1-NOV-1996 (TrembLrel. 01, Last sequence update)
Q1-NOV-1999 (TrembLrel. 12, Last annotation update)
COMPLEMENT RECEPTOR 1.
Homo sapiens (Human).
Eukaryota; Metaga; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
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                                                                                                                                                                                                                                                       300 PRCTLKPCD 308
                                                                                                                                                                                                                                                                                              351 PTCEVKSCD 359
                                                                                                                                                                                                                                                                                                                         245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 YPEGTOAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG 82
                                                                                                                                                                                                                                                                                                                                                              S-RVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                           IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCOPGFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L17402;
L17403;
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Similarity 31.4%;
97; Conservative
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AAB60694.1;
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                            Chordata; Craniata; Vertebrata; Mammalia;
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Submitted
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J. Immunol. 151:6214-6224(1993).
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VIK D.P., WONG W.W.;
                                                                                                                                                                                         63 FPIGTYLNYECRPGYSGRPFSI-ICLKNSVWTGAKD-R-CRRKSCRNPPDPVNGMYHVIK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                      83
                                                                                                                                                                     24 YPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTG
                                                                                                                                                                                                                                                 Local
EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                      FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 233
                                                                                                                                        G-I-QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTIT-NGD 176
                                                                                                             GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
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L17402;
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L17427; AAB60695
L17428; AAB60695
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97; Conser
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ilarity 31.4%;
Conservative
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272846 MW; 5869B6F9 CRC32;
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                                                                                                                                                                                                                              Score 409; DB 4; Le
Pred. No. 2.64e-77;
66; Mismatches 110;
                                                                                                                                                                                                                                                          Length 2489;
                                                                                                                                                                                                                               Indels
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RESULT AND RESULT STATES OF THE STATES OF TH
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01.NOV-1996 (TIEMBLIEL. 01, Created)
01.NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01.NOV-1999 (TIEMBLIEL. 12, Last annotation update)
COMPLEMENT RECEPTOR 1 PRECURSOR (FRAGMENT).
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SEQUENCE
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J. Immunol. 153:691-700(1994).
EMBL; L24921; AAA51439.1; -.
HSSP; P10998; 1VVC.
PFAM; PF00084; sushi; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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BIRWINGHAM D.J., SHEN X.P., HOURCADE D., NICKELLS M.W., ATKINSON J.P.;

"Primary sequence of an alternatively spliced form of CR1. Candidate
for the 75,000 M(r) complement receptor expressed on chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Alternative splicing.
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                                                                                                                         245 EEKSCDNP-YIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTA-KCTSTG-WIPA- 299
                                                                                                                                                                269 S-RYCQPPPDYLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASLRCTPQGDWSPAT 325
                                                                                                                                                                                                                                                     189 EIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                              139 IVSSAMEPDREYHFGQAVRFVCNSGY---KI-E--GDEEMHC-S-DD--GFWSKEKPKCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                  152 FISTNRE-N--FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 208
                                                                 326 PTCEVKSCD 334
                                                                                                                                                                                                                                                                                                                   209 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPPRVKCQALNKWEPELPSC 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 15.9%; Score 403; DB 6; Length 661;
Local Similarity 31.1%; Pred. No. 1.07e-75;
Les 96; Conservative 66; Mismatches 111; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 GNVFEYGVKAVYTCNEGYQLLGE--INYREC-DTDGWTNDIPICEVVKC-LPVTAPENGK 138
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   PRCTLKPCD 308
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72966 MW;
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COMPLEMENT RECEPTOR 1.
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Search completed: Thu Jun Job time: 34 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:49:10 2000; MasPar time 13.73 Seconds 738.315 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-316-163-14 (1-428) from US09316163.pep 3371

Sequence: 1 EDCKGPPPRENSEILSGSWS......DTYYCTENGWSPPPKCVRIK 428

Scoring table:

PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%/ Listing/first 45 summaries Database: a-geneseq36 1:geneseqp

Mean 34.511; Variance 134.258; scale 0.257

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

439 130 543 1 R28558 CR1-4 (109N, 110A, 111 9.31e-	Result NO. 1 2 3 4 4 5 7 7 8 8 9 10	Score 1385 1276 712 537 445 446 446 446 446 441	Query Match 47.1 37.9 21.1 15.9 21.3 2.1 13.2 13.2 13.2 13.2 13.2 13.2	Length 240 216 578 581 543 543 776 1930 2317 543 543	DB	W39154 W39155 Y09065 R13490 R28557 R28557 W45899 P28553 R28553	cription an partial Compl an partial Compl an complement fa an C4 binding pr -4 (99H, 103E) a -4 (78T, 79D) a no acid sequence an complement re protein -4 (85R, 87N) an -4 (114S) analog	Pred. No. 1.86e-13 1.46e-12 1.36-13 1.42e-12 1.36-13 2.21e-33 2.21e-33 1.74e-33 1.74e-33 1.74e-33 1.74e-33 3.31-33
	15 16	439 439	13	1537 2039	بر بر	R11982 R36743	Partial human compleme CR1.	
439 13.0 1537 1 R11982 Partial numan compleme 9.31e-	17	437	13	2039	سر مــر	R11810 R28547	an complement	1.50e-3 1.91e-3
439 13.0 1537 1 R11982 Partial numan compleme 9.31e- 439 13.0 2039 1 R36743 CR1. 439 13.0 2039 1 R11810 Human complement type 1.50e- 437 13.0 2039 1 R128547 CR1-4 (528, 538, 549) 1.91e-	19	436	12	543	ر بر	R28569	-4 (369-376 ST	Ľ
439 13.0 1537 1 R11982 Partial numan compleme 9.3 439 13.0 2039 1 R36743 CR1. 437 13.0 2039 1 R11810 Human complement type 1.5 436 12.9 543 1 R28547 CR1-4 (525, 535, 54P) 1.5 436 12.9 543 1 R28569 CR1-4 (369-376 STKPPIC 1.5	20	436	12	543	ш	R28568	4-	1.91e-
439 13.0 1537 I R11982 Partial numan compleme 9: 439 13.0 2039 I R36743 CR1. 437 13.0 2039 I R11810 Human complement type 1: 436 12.9 543 I R28547 CR1-4 (352s, 535, 54P) 1: 436 12.9 543 I R28568 CR1-4 (369-376 STKPPIC 1: 436 12.9 543 I R28568 CR1-4 (3677, 349Y) ana 1:		435	12	543	ᆫ	R28555	-4 (	2.42e-
439 13.0 1537 1 R11982 Partial numan compleme 9.34e 439 13.0 2039 1 R36743 CR1. 437 13.0 2039 1 R11810 Human complement type 1.50e 436 12.9 543 1 R28547 CR1-4 (528, 538, 54P) 1.91e 436 12.9 543 1 R28569 CR1-4 (369-376 STKPPIC 1.91e 436 12.9 543 1 R28568 CR1-4 (347T 3.49Y) ana 1.91e 436 12.9 543 1 R28555 CR1-4 (92T) analogue. 2.42e-	21	5		1		1		
13.0 1537   R11982 Partial numan compleme 9.3481 13.0 2039   R36743   CR1. 9.316- 13.0 2039   R11810   Human complement type 1.50e- 12.9 543   R28547   CR1-4 (525, 538, 54P)   1.91e- 12.9 543   R28569   CR1-4 (369.376 STKPPIC 1.91e- 12.9 543   R28568   CR1-4 (347T, 349Y) ana 1.91e- 12.9 543   R28555   CR1-4 (92T) analogue. 2.42e- 12.9 543   R28565   CR1-4 (121Q) analogue. 3.08e-	21 22	404	7	543	_	R28565	-4 (1210)	3.08e-

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121 INGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNG 180

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44	43	42	41	40	39	38	37	36	ω 5	34	<b>ω</b> ω	32	31	30	29	28	27	26	25	24
363 363	379	389	390	411	416	422	422	423	424	425	426	427	428	430	430	431	431	432	432	433
10.8	11.2	11.5	11.6	12.2	12.3	12.5	12.5	12.5	12.6	12.6	12.6	12.7	12.7	12.8	12.8	12.8	12.8	12.8	12.8	12.8
254	263	577	830	579	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543
	μ.	Н	1	<b>-</b>	ب	μ.	<b> </b>	Н	٢	ب	<b>-</b>	1	_	-ب	۳		<u> </u>	Н	Н	_
R47155	P92003	W06882	R65216	W39924	R28546	R28543	R28559	R28554	R28556	R28567	R28564	R28548	R28544	R28562	R28545	R28551	R28561	R28563	R28549	R28570
sequence of soluble co	sequence or	שי		Amino acid sequence of	, 47D, 491	-4 (35E, 37Y)	-4 (114-117ST)	-4 (92T, 94H) ana	-4 (94H)	-4	-4 (116K, 11/P) an	-4 (57V, 5	-4 (35E)	3	-4 (37Y) a	-4 (	4	_	-4 (64K	-4 (266-274 K
6.46e-25		86-7		7.44e-30	່, ເ	.4Le-3	.41e-	4.260-31	. 35e-	.64e-		1.64e-31	1.298-31	8.01e-32		. sue-s	. 30e-3		. 900	.91e-

#### ALIGNMENTS

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RESULT
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AC YC
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TAC WAS

AC WA
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09-APR-1997; U5-812481.

06-MAR-1997; U5-815083.

09-APR-1996; U5-630048.

06-MAR-1997; U5-038614.

06-MAR-1997; U5-038614.

(BARD-) BARD DIAGNOSTIC SCI INC.
Enfield DL, Hass GM, Kinders RJ;
WPI; 97-512742/47.

WP-PSDB; V02791.
                                                                                                                                                                           Human complement factor H homolog protein.

Human complement factor H; immunological mechanism; complement reaction; gene therapy; immune stimulation; haematopolesis regulation; chemotactic; tissue growth activity; anti-inflammatory; tumour inhibition;
                                                                                                                                                      secretory signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating or screening for cancer, e.g. renal or urogenital cancer - by modulating or detecting tumour associated human complement Factor H related antigen, or nucleic acid encoding it Example 6B; Fig 6B; 104pp; English.

This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour-associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                        02-OCT-1998; J04448
                                                                                           WO9918200-A1.
                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                       06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                               Y09065 standard; Protein; 578
                                                               15-APR-1999.
                                                                                                                                                                                                                                                                                                                                                              Y09065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9738136-A1.
16-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone prrB9FH410 CFH related protein fragment. Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W39155 standard; Protein; W39155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       urogenital cancer; medicament; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 VVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPPRVENGDGIYLKPVYKENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AVRFVCNSGYKIEGDEEMHCSDDGFWGKEKPKCVEISCKSPDVINGSPISQKIIYKENER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 DYSPLRIKHRIGDEITYQCRNGFYPATRGNTAKCISIGWIPAPRCILKPCDYPDIKHGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 37.9%;
Local Similarity 73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPYTAPENGKIVSSAMEPDREYHFGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCDEGYQLLGEIDYRECDADGWTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAPRCSLKPCDFPQFKHGRL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLTPYIPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AA;
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1276; DB 1;
Pred. No. 1.44e-122;
26; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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(PROT-) PROTEGENE INC.
(SAGA) SAGAMI CHEM RES CENT.
KATO S, Sekine S;
WPI; 99-264019/22.
N-PSDB; X34737.
                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-1991 (first entry)
Human C4 binding protein.
C4bp; monomer; complement protein; pJOD.C4bp.3;
                                   region
                                                                                                     region
                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 short consensus repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA encodes a protein having homology to human complement factor H, which plays a role in the immunological mechanism involving the complement reaction. The protein can also be used as an antigen for preparing antibodies against the protein. The count can be used as a probe for gene diagnosis and the gene for gene therapy, as well as for large-scale expression of the protein. The protein may also have immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, anti-inflammatory activity, tumour inhibition activity, chemotactic/chemokinetic activity receptor/ligand activity, etc. The protein is identified by the presence of a hydrophobic N-terminal secretory signal region, knowledge of the protein function is not required, as in e.g. methods of expression
                                                                                                                                                                    region
                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R13490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R13490 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 EYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDT--YYCTENGWSPPPKCVRI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 ENGFISESSSIYILNKEIQYKCKPGYATADGNSSGSITCLQNGWSAQPICIKF 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 MWFKLHDTLDYECYDGYESSYGNTTDSIVCGEDGWSHLPTCYNSSESCGPPPPISNGDTT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 ILNEETQYNCKPGYATADGNSSGSITCLQNG-WSTQ-PICIKF-CDMPVFENSRAKS-NG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claims 1; Page 55-58; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 YYCDQNFVTPSGSYWDYIHCTQDGWSPTVP-C-LRTCSKSDVEIENG-FIS---ESSSIY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YENTRRPYFPVATGQSYSYYCDQNFVTPSGSYWDYIHCTQDGWLPTVPCLRTCSKSDIEI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V-YKENERFQYKCKQGF--VYKERGDA-VCTGSGWNPQPSC-EEM-TC-LTPYIPNGIYT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFGQVVRFECNSGF-KIEGQKE--MHCSENGLWSNEKPQCVEISCLPPRVENGDGIYLKP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLRQCI-FHY-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHRIKHRID-DEIRYECKNGFYPATRSPVSKCTITGWIPAPRC-SLKPCDFPQFKHGRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFPQKVYLPWSRVEYQCQS-YYELQGSKYVTCSNGDWSEPPRCISMKPCEFPEIQHGHLY 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTCDEGYQLL-GEI-DYRECDADGWINDIPICEVVKCL-PVTELENGRIVSGAAEPDQEY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 35.1%; 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578 AA;
/label=
                                                               /label= SCR7
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                              'label- SCR8
                                                                                                                                                                 /label= C4bp
33. .93
                                                                                                                                                                                                                                                                   /label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.1%;
                                                                                                  . 155
                               .219
                                                                                                                                                                                                                                   581
                                                                                                                                                                                                                                                               l= signal_peptide
SCR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 712; DB 1; Length 578;
Pred. No. 1.36e-61;
72; Mismatches 127; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
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Gaps 25;

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맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New C4 binding protein fusion proteins and DNA encoding them comprise assemblies of C4bp monomers linked to functional molety, e.g. AZI, useful as delivery vehicles in diagnosis and therapy Example 1; Fig 1; 105pp; English.

This sequence was deduced from human hepatocyte (Hep G2) cDNA obtained following PCR amplification. The protein is a monomer containing 8 SCRs. Each SCR forms a looped domain due to the presence of two intradomain disulphide bonds (only the disulphide bonds of SCR8 are labelled in the Features Table). Within each SCR, the first cysteine residue bonds with the third and the second cysteine residue bonds with the third and the second cysteine residue bonds with the fourth. This secondary structure is responsible for the conformational flexibility of the C4bp monomer. The invention covers fusion proteins in which the monomer sequence, or a specified subfragment of it, e.g. having 5, 4, 3 or 1 SCR(s) is fused to the C-terminal of a protein such as a viral receptor, coutoffice the contain and contains the immunogen, enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOG-) BIOGEN INC.
Pasek MP, Winkler G, wiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-1991;
378
                                                                                                                                                                                                                                116 WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS
                                                                                                                                                                                                                                                               147
                                                                                                                                                                                               203 VENETIGVWRPSPPTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSV 262
                                                                                                                                                                                                                                                                                                                                                                                                                              Match 15.9%;
Local Similarity 30.7%;
les 138; Conservative
                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                                                               33 NC-GPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNT
                                                                                                                                                                                                                                                                                                                                                                N
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                                                                                                                              IHCDADSKWNPSPPACEPNSCINLPDIPHASWETYPRPTKEDVYVVGTVLRYRCHPGYKP 322
                                                                                                                                                                                                                                               SRICRKRPCGHPGDTPFGSFRLAVGSEFBFGAKVVYTCDEGYQLLGEIDYR-EC-DAD-G
                                                                                                                                                                                                                                                                                                                   FCIY-KR-CRHPGELRNG--QVEIKTDLSFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVG
                                                                                                                                                                                                                                                                                                                                                                DCKGPPPREN-SEILSGSWSEQLYSEGTQATYKCRPGY-RTLGTIVKVCK-NGEWVPSNP 58
EISFSCHETSRFSAI-CQGDGTWSPRTPSCGDICNFP-PKIAHGHYKQSSSYSFFKEEII 435
                                                              TIDEPTIVICOKNLRWIPYOGCEALCCPEPKLNNGEIT-QH-RKS-RPANHC-VY-FYGD
                                                                                                AVC-TGSGWNP-QPSCEEMTCLT-PYIPNGIY-T-PHRIKHRI--DDEI-RYECKNGFYP
                                ATRSPVS-KCTIT-GWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCD
                                                                                                                                                                -EN---GLWSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin, e
581 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .279
/label= SCR5
280. .345
'label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65. .92 /note= "intradomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= C4bp_core
/note= "responsible for multimer assembly"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etc. See also Q13243-51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCR4
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "intradomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TR;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 537; DB 1; Le
Pred. No. 5.15e-43;
85; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                  The cDNA clone designated CRI-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CRI. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CRI-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CRI-4 sequence; the sequence given here was constructed from the full-length CRI amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR1-4 (99H, 103E) analogue.
short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R28557 standard; peptide; R28557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Atkinson JP, Hourcade D, WPI; 92-375009/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for diagnosis etc.
Claim 11; Fig 2 and R11810; 23pp; English.
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(UNIW ) UNIV WASHINGTON.
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11-NOV-1992
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83
                                                                                                                                       77
                                                                                                                                                                                               22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QCHSGYSLPNGQDTYYCTENGWSPP-PKC
                                           RIVSGAAEPDQEYYFGQVVRFECN-
                                                                                                                                    IKGIOFGSQIKYSCTKGYRLIGHSS-AECIISGDTVIWDNETPICDRIPCGLPPT-ITNG 134
                                                                                                                                                                  YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV
                                                                         DFIS--THRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC
                                                                                                       GSEFEFGAKVVYTCDEGYQLLGEIDYREC--DADG--WTNDIPICEVVKC-LPVTELENG
                                                                                                                                                                                                                               105;
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                          543 AA;
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                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Ser substituted 103
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451. .510
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                                                                                                                                                                                                                                            13.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543
                                                                                                                                                                                                                            Score 445; DB 1;
Pred. No. 2.21e-33;
72; Mismatches 106
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                                           -SGF-KI-E--GQKEMHC-S
                                                                                                                                                                                                                               Mismatches 106; Indels 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glu (SCR-9)"
                                                                                                                                                                                                                                                            Length 543;
                                               -EN--GLWSNEKPQC
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                                               187
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosis etc.

Claim II; Fig 2 and R11810; 23pp; English.

The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988)

168:1255-1270. It encodes the first 8 and a half amino terminal

SCRs of CR1. The invention concerns analogues of "regulator of

complement activation" proteins or truncated, hybrid or recombinant

forms of them. CR1-4 is a preferred truncated form and a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type I receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant reject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-1992; 303826.
03-MAY-1991; US-695514.
(UNIW ) UNIV WASHINGTON
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19-MAR-1993
                139
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                                                                                                                                                                                               77
                                                                                                                                                                                                                                                         24
                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                       FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                       FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92-375009/46.
IVSGAADODQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                                                        GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                               ITDIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-IINGD 135
                                                                                                                                                                                                                                            YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSRV-COPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PS 243
                                                                                                                                                                                                                                                                                                                                                                                     103;
                                                                                                                                                                                                                                                                                                                                                                              h 13.2%;
Similarity 32.0%;
103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Lys substituted by Thr (SCR-9)"
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511. 543
/label SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Gly substituted by Asp (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= SCR-2
451. .510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= SCR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCR-9
                                                                                                                                                                                                                                                                                                                                                                           Score 445; DB 1; L
Pred. No. 2.21e-33;
74; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 543;
                                                                                                                                                                                                                                                                                                                                                                              Indels 38;
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is an amino acid sequence of the human soluble complement receptor 1 (SCR1), useful in the treatment of T-cell or B-cell mediated immune responses. It is used to inhibit a T-cell or B-cell-mediated immune response to prevent immune response-mediated tissue rejection and destruction or clearance or inactivation of an expressed protein especially from cells that have been treated by get
                                                                                                                                                                                                                                                                                                                                                                                                                                                   an interferon gamma secretory response, autoimmune response or neurological response, e.g. Alzheimer's or Parkinson's disease or multiple sclerosis. Also the protein can be used to treat systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of the soluble complement receptor 1 (sCR1). Human; soluble complement receptor 1; sCR1; T-cell; B-cell; mediated immune response; inhibition; tissue rejection; gene therapy; dystrophin; inflammatory response; interferon-gamma secretory response; autoimmune response; neurological response; Alzheimer's disease; parkinson's disease; multiple sclerosis; systemic lupus erythematosus; remainded arthritis; myasthenia gravis; epidermis bullosa;
                                                                                                                                                                                                                                                                                                                                                                                                                    epidermis bullosa or Hashimoto's disease. Sequence 778 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy to express the protein, e.g. dystrophin. The protein can also be used to inhibit a T-cell or B-cell-mediated inflammatory response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragment of soluble human complement receptor 1 - useful treating T-cell or B-cell mediated immune responses e.g. inflammatory responses such as rheumatoid arthritis Disclosure; Fig 1, 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Annenkov A, Chernajovsky Y; WPI; 98-568350/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-1998; G01012.
05-APR-1997; GB-006950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hashimoto's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W73147 standard; protein; 778 AA
239 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                  83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                             24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV
                                                                                                                                                                                                                                                                          68 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 122
                                                                                                                                                                                                                                                                                                                       Match 13.2%;
Local Similarity 32.3%;
tes 104; Conservative
                                          IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                     FIS--THRE-NEHYGSVVTYRCHPGSGGRKVFELVGEPSIYCTSHDDQVGIWSGPAPQCI
                                                                                                                                                                                IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                       Score 446; DB 1;
Pred. No. 1.74e-33;
72; Mismatches 108
                                                                                                                                                                                                                                                                                                                       Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The protein can also
                                                                                                                                                                                                                                                                                                                       Indels 38;
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189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC

244

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Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane-binding elements (MBE) of low membrane affinity covalently associated with (I). MBE interact, independently and with thermodynamic additivity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (I) itself, specifically inflammation or any other complement-related disorder (e.g. neurological disease, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others; including application to indwelling devices) and thrombolytic disease, but also to treat allergy, induce weight loss, to treat ischaemia or asthma and as immuno-modulators for treating multiple sclerosis. (A) are administered orally, topically, by injection or inhalation at 0.01-10 (preferably 0.1-10) moderniary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human complement receptor 1 (residues 1-1929).

Membrane binding element; thrombotic disease; soluble protein; complement-related disease; integral membrane protein; inflammation; short consensus repeat; SCR 1-3; CR1; complement receptor type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-1998.
08-JUL-1997; E03715.
15-JUL-1996; GB-014871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents human complement receptor 1 (CR1, CD 35) N-terminal fragment. The invention relates to a soluble derivative (A) of a soluble polypeptide (I), which comprises at least 2 heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross_links
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W45899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derivatives of soluble poly:peptide(s) bonded to low affinity membrane binding groups - useful for treating complement-rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 98-110524/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dodd I, Mossakowska DEI, Smith RAG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombotic diseases, providing improved localisation at cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ADPR-) ADPROTECH PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Pages 60-61; 75pp; English.
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                                                                                                                                                                136 FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
253 SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                       189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1-10) mg/kg/day.
equence 1930 AA;
                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                      24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                              22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                 Match 13.2%;
Local Similarity 32.3%;
es 104; Conservative
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                                                                               I PNKCTPPNVENGILVSDNRSLFSLNEVVEFRCOPGFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                                       GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                               IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                        IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1930
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in W45889"
                                                                                                                                                                                                                                                                                                                                                                            Score 446; DB 1; Length 1930;
Pred. No. 1.74e-33;
72; Mismatches 108; Indels 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences encoding new CR1 protein - and its fragment, for diagnosis and control of complement-related immune defects, inflammation, myocardial infarct, etc Claim 1, fig. 1, 191pp; English.
This is full-length CR1 protein, and shortened forms are new, lacking This is full-length CR1 protein, and shortened forms are new, lacking This is full-length CR1 protein, and shortened forms are new, lacking This is full-length CR1 protein, and shortened forms are new, lacking This is full-length CR1 protein.
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(TCEL) T Cell Sciences Inc; (UYJO) The Johns Hopkins University; (BRIG*) The Brigham and Women's Hospital.
Fearon DT, Klickstein LB, Wong W, Carson G, Concino MF, Makrides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CR1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P92219 standard; protein; 2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the transmembrane region. The proteins and fragments bind C3b and/or C4b, have cofactor activity and inhibit C3 and C5 convertase activity. In the sequence, x=untranslated region. This has 7 short consensus repeats (CR) of 4 long direct homologous repeats (CR) (See fig. 10 in patent). Deletion mutants, eg LHR-A for binding of C4b, and LHR-C for C3b binding, be made, and LHR-B and C can detect CR2 sequences. They are useful in diagnosing and treating immune disorders, and preven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; N91477
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01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO8909220-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 89-309498/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       perfusion injury.
Sequence 2317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                        186 FIS--TNRE-NFHYGSYVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 242
                                                                                                                                                                                                                                                                                                                                                                         127 IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 185
                                                                                                                                                                                                     243 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
300 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                  83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                                                                                                                                                   24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                            EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                                EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                         PTCEVKSCDDFMGQLLNGRVLF 381
                                                                                                                        SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA
                                                                                                                                                                                                                                                 IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%;
Similarity 32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cofactor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U01358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 446; DB 1;
Pred. No. 1.74e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and prevent
                                                                                                                                                                                                                                                              188
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RESULT ID R

T 10 R28553 standard;

peptide;

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Pr Calaim 11; Fig 2 and R11810; 23pp; English.

CC The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988)

CC 168:1255-1270. It encodes the first 8 and a half amino terminal

CC SCRs of CR1. The invention concerns analogues of "regulator of

CC complement activation" proteins or truncated, hybrid or recombinant

CC complement of them. CR1-4 is a preferred truncated form and a number of

CC specified substitution variants of it are claimed in which certain

CC specified substitution variants of it are claimed in which certain

CC specified of 3bb- and C4b-binding are substituted by amino acids from

CC degree of C3b- and C4b-binding are substituted by amino acids from

CC contain the CR1-4 sequence; the sequence given here was constructed

CC contain the CR1-4 sequence; the sequence having GENESEO

CC accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
300 PRCSLKPCD-F-PQFKHGRLYY 319
                                         310 PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                      189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating auto: immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Atkinson JP, Houre WPI; 92-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_difference 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP-512733-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1993 (first entry)
CR1-4 (85R, 87N) analogue.
Short consensus repeat; regulator of complement activation;
C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R28553;
19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                        22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                  24
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                     SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                     EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                                          IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC 252
                                                                                                                                                                                                              IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV 188
                                                                                                                                                                                                                                               FIS--TNRE-NFHYGSVYTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                   IKGIQFGSRINYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                                                                                                                                                                                                                                                      YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                   GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                     103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-695514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Lys substituted by Asn (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= SCR-1
61. .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Gln substituted by Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= SCR-8
511. .543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 441; DB 1;
Pred. No. 5.77e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                              73; Mismatches 108; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or for diagnosis etc.

T for diagnosis etc.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Chaim 13; Fig 2 and R11810; 23pp; English.

Chaim 14; Fig 2 and R11810; 23pp; English.

Chaim 15; Fig 2 and R11810; 23pp; English.

Chaim 16; Fig 2 and R11810; CR1-4 was described in J.Exp.Med.(1988)

Consider the invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of complement etc. A specified substitution variants of it are claimed in which certain consistent in SCR-2 which have been identified as important for the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1992.
28-APR-1992;
03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
300 PRCSLKPCD-F-PQFKHGRLYY 319
                              310 PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                      189
                                                                                                                                                            193 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                                                                                                                                                                              139 IVSGAAEPDQEYYFGQVVRFECN--SGF-KI-E--GQKEMHC-S-EN--GLWSNEKPQCV
                                                                                                                                                                                                                            136 FIS--THRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 92-375009/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R28560;
19-MAR-1993 (first er
CR1-4 (114S) analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating auto:immune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atkinson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R28560 standard; peptide; 543 AA
                                                                                                                                                                                                                                                             83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                            77 IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWSNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                                                                                                                                                                                                                               24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                                                               22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                          EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                          SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA
                                                                                                                            EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                          103;
                                                                                                                                                                                                                                                                                                                                                                                                                      h 13.0%;
Similarity 32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-695514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Asp substituted by Ser (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= SCR-2
451. .510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label = SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                    Score 439; DB 1;
Pred. No. 9.31e-33
73; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to suppress transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 108; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 543;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1993 (first entry) CR1-4 (109K, 110A, 111A, 112H) analogue. CR1-4 (109K, 110A, 111A, 112H) analogue. short consensus repeat; regulator of complement activation; c3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Asp substituted by Asn (SCR-9)" misc_difference 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R28558 standard; peptide; 543 AA. R28558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 11-NOV-1992.
28-APR-1992; US-695514.
03-MAY-1991; US-695514.
(UNIW ) UNIV WASHINGTON.
Atkinson JP, Hourcade D, Krych M;
WPI; 92-375009/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                                                                                                                                           Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_difference 112
                                                                                                                                                                                                                Sequence
                                                                                                        77
                                                                                                                           24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                    IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC 252
                                                     FIS--TNRE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                       IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGNAAHWDNETPICDRIPCGLPPT-ITNGD 135
 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                         GSEFEFGAKVVYTCDEGYQLLGE--IDYREC-DADGWINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                   543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note "Ile substituted by His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Val substituted by Ala (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Thr substituted by Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451. .510
/label= SCR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "TRUNCATED"
                                                                                                                                                                                  13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .543
                                                                                                                                                                      Score 439; DB 1;
Pred. No. 9.31e-33;
72; Mismatches 109
                                                                                                                                                                         Mismatches 109;
                                                                                                                                                                                              Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCR-9)"
                                                                                                                                                                          Indels
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                                                                                                                                                                                                              Вþ
                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                Example 8; Page 18 and Ril810; 23pp; English.

Example 8; Page 18 and Ril810; 23pp; English.

168:1255-1270. It encodes the first 8 and a half amino terminal conservation of the first 8 and a half amino terminal complement activation proteins or truncated, hybrid or recombinant complement activation variants of it are disclosed in which certain specified substitution variants of it are disclosed in which certain specified substitution variants of it are disclosed in which certain specified substituted by amino acids from the corresponding positions in SCR5 which are involved in C3b-and the corresponding positions in SCRs which are involved in C3b-binding. The substitution variant given here has increased C3b-binding. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1993 (first entry)
CR1-4 (364-367 NAAH) analogue.
cR1-4 (364-367 NAAH) analogue of complement activation;
short consensus repeat; regulator of complement type 1 receptor.
C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R28571 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region
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28-APR-1992; 303826.
03-MAY-1991; US-695514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference 364. .367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Atkinson JP, Hourd WPI; 92-375009/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating auto:immune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosis etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON
                                                                                                                                           77
                                                                                                                                                                         24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV
                                                                                                                                                                                                          22 FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCRNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                 Match 13.0%;
Local Similarity 31.9%;
les 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTCEVKSCDDFMGQLLNGRVLF
IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPVFVMKGPRRVKCQALNKWEPELPSC
                                    FIS--TURE-NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                       GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                        IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD
                                                                                                                                                                                                                                                                                                                         543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "MESL substituted with NAAH from SCR-8-9 to increase C3b binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= SCR-9
/note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= SCR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCR-9
                                                                                                                                                                                                                                                   Score 438; DB 1; Le
Pred. No. 1.18e-32;
79; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to suppress transplant rejection,
                                                                                                                                                                                                                                                                                         Length 543
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                          48;
                                              188
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RESULT
ACC 
                                                                                                                                                                                                                                                                                                                                                                                                            or for diagnosis etc.

Staim 11; Fig 2 and R11810; 23pp; English.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 11; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 12; Fig 2 and R11810; 23pp; English.

Claim 14; Fig 2 and R11810; 23pp; English.

Claim 20; Fig 3 and All Fig 3 and All famino terminal complement activation; proteins or truncated, hybrid or recombinant complement activation; proteins or truncated form and a number of Complement activation variants of it are claimed in which certain compositions in SCR-2 which have been identified as important for the Complement of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atkinson JP, Hourd
WPI; 92-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-NOV-1992.
28-APR-1992; 303826.
03-MAY-1991; US-6955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR1-4 (64K) analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R28550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R28550 standard; peptide; 543 AA
83 GSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--WTNDIPICEVVKC-LPVTELENGR 138
                                                                                        77
                                                                                                                                                      24
                                                                                                                                                                                                                                                                             Local Similarity tes 103; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 CTVNGWEPEVP-C 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 SRV-COPPEDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 GNAAHWNSSVPVC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 135
                                                                                                                              YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                           FPIGTYLNYECRPGYSGR-PFSIICLKNSVWTGAK-DR-CRRKSCKNPPD-PVNGM-VHV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRCSLKPCDFPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGF--TTPSQSYWDYLR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTCEVKSCD--DFM-GQLL--NGR-VLFPVNLQLGAKVDFVCDEGFQLKGSSASY-CVLA 362
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                                                                                                                                                                                                                                                                                                                                                                                                        543 AA;
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-695514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
511. .54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Arg substituted by Lys (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= SCR-2
                                                                                                                                                                                                                                                                                                     13.0%;
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                                                                                                                                                                                                                                                                       Score 437; DB 1;
Pred. No. 1.50e-32;
72; Mismatches 109
                                                                                                                                                                                                                                                            Mismatches 109; Indels 38;
                                                                                                                                                                                                                                                                                                                                 Length 543;
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Š В δ 밁

ρ

В

461 FPIGTSLKYECRPEYYGR-PFSITCLD-NLVWSSPKDVCKRKSCKTPPD-PVNGM-VHVI 516

24 YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG 83

Matches

Conservative

Score 439; DB 1; Pred. No. 9.31e-33; Mismatches

Length 1537; Indels 38;

106;

Gaps

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В
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                       Query Match
                                                                                        Human complement receptor type 1 gene, encoded proteins and fragments - for treatment of immune disorders, myocardial infarct, damage due to inflammantion and in treatment of thrombosis Disclosure; Fig 5; 234pp; English.

This sequence comprises three of the four tandem, direct, long homologous repeats of the full-length F allozyme of CRI. LHR-A is absent. Each LHR might represent a single C3b/C4b binding domain, making the receptor multivalent. The LHR's are composed of 7 short consensus repeats of 60-70 residues resembling the SCR's of other consensus repeats of 60-70 residues resembling the SCR's of other 23/C4 binding proteins. The protein and fragments of it having C3b and/or C4b binding activity can be used to treat immune disorders
                                                   Sequence
                                                                            or disorders involving inappropriate complement activity.
                                                                       See also Q11642.
                                                                                                                                                                                                                                                                                                                   (TCEL-) T CELL SCI INC.
(UTGO) JOHNS HOPKINS UNIVERSITY.
(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
FEATON DT, Klickstein LB, Wong WW, Carson GR, Hoh M, Concino Makrides SC, Marsh HC;
                                                                                                                                                                                                                                                                                            N-PSDB; Q11643
                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-1991.
25-SEP-1990; U05454.
26-SEP-1989; US-412745.
26-SEP-1990; US-912349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9105047-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune response; long homologous repeat; LHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial human complement type 1 receptor. complement system; C3b/C4b receptor; CR1; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1991 (
Partial human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R11982 standard; Protein; 1537 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R11982;
Match 13.0%;
Local Similarity 32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 PTCEVKSCDDFMGQLLNGRVLF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 SRV-COPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASMRCTPQGDWSPAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 FIS--TNRE-NFHYGSVYTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
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/note= "has 67 per cent homology to site of protein kinase C phosphorylation in the EGF receptor"
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439. .891
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/note= "positively-charged; preceded by hydrophobic
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Tabular output not generated. Run on: MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd >US-09-316-163-14 (1-428) from US09316163.pep 3371 1 EDCKGPPPRENSEILSGSWS......DTYYCTENGWSPPPKCVRIK 428 Thu Jun 8 21:49:45 2000; MasPar time 24.14 Seconds 836.361 Million cell updates/sec

Description: Perfect Score:

Sequence:

Scoring table: PAM 150 Gap 11

Searched:

142080 segs, 47172406 residues

Post-processing: Midfmum Match 0% First 45 summaries Statistics: Database: Mean 45.494; Variance 73.749; scale 0.617 pir62 1:pip1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

2222210 23322222222222222222222222222222	Result No.
2834 2339 2389 2389 11720 11129 11129 646 646 646 646 647 447 449 449 444 447 446 447 446 447 446 447 446 447 446	Score
70.99 70.99 33.07 33.57 33.57 33.57 119.22 114.77 114.77 114.77 113.33 113.33 113.33 113.33 113.29	Query Match
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complement factor H p complement factor H p complement factor H p complement factor H p factor H - bovine (fr complement factor H-r complement factor H-r apolipoprotein H-rela complement factor H-r complement chain protein a C4BP protein alpha ch C4BP protein alpha ch C4BP protein H-rela complement C3b recept apolipoprotein H-rela complement receptor 1 complement receptor 1 complement C3b/C4b re complement factor H-r factor H homolog - hu factor H homolog - hu C4b-binding protein a	Description
0.00e+00 0.00e+00 0.00e+00 0.00e+00 5.17e-249 1.40e-152 1.28e-126 5.32e-126 2.32e-126 2.52e-199 8.78e-89 8.78e-89 8.78e-89 8.78e-84 6.17e-84 6.17e-84 6.17e-84 6.17e-77 1.82e-77 1.82e-77 1.82e-77 3.17e-74	Pred. No.

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384	377	369	668	610	618	612	610	345	345	263	768	768	345	830	263	482	497	579	560	243	270	
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membrane cofactor pro	membrane cofactor pro	membrane cofactor pro	coagulation factor XI	endothelial leukocyte	E-selectin precursor	endothelial leukocyte	endothelial leukocyte	apolipoprotein H prec	apolipoprotein H prec	complement control pr	P-selectin precursor	P-selectin - rat	apolipoprotein H prec	P-selectin precursor	apolipoprotein H homo	complement C3b/C4b re	complement regulatory	sperm-egg recognition	hypothetical protein	complement factor H-r	complement factor H-r	
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808-861
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509-564
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85-141
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121 PICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLW 180
                         139 PLCEVVKCLPVTELENGRIVSGAAETDQEYYFGQVVRFECNSGFKIEGHKEIHCSENGLW 198
                                                                61
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Local Similarity 83.0%;
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                                                       ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDI 120
                                                                                                              EDCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSR 60
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                                                                            ICRKKPCGHPGDTPFGSFRLAVGSQFEFGAKVVYTCDDGYQLLGEIDYRBCGADGWINDI 138
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#length 1234 #molecular-weight 139081 #checksum 3676
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                                                                                                                                                                                                                                                                     #authors Day, A.J.; Ripoche, J.; Lyons, A.; McIntosh, B.; Harris,
T.J.R.; Sim, R.B.
#journal Biosci. Rep. (1987) 7:201-207
#title Sequence analysis of a cDNA clone encoding the C-terminal end
#cross-references MUID:88025472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.
#journal Eur. J. Immunol. (1991) 21:799-802
#title Human complement factor H: two factor H proteins are derived
#cross-references MIID:91184292
#cross-references MIID:91184292
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                                                                                                                           ##residues 'DFRN',579-1231 ##label DAY ##cross-references GB:M17517; NID:g180497; PIDN:AAA52076.1; PID:g180498 ##note parts of this sequence were determined by protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-1231 ##label RIP 1-1231 ##cross-references EMBL:Y00716; NID:g31964; PIDN:CAA68704.1; PID:g31965 ##note 402-Tyr was also found parts of this sequence, including the amino and carboxyl ends of the mature protein, were confirmed by protein
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Ripoche, J.; Day, A.J.; Willis, A.C.; Belt, K.T.; Campbe R.D.; Sim, R.B.
Biosci. Rep. (1986) 6:65-72
Partial characterization of human complement factor H by
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#journal #title

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#title
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#title Cloning of the 1.4-kb mRNA species of human complement factor
H reveals a novel member of the short consensus repeat
family related to the carboxy terminal of the classical
150-kDa molecule.
#cross-references MUD:91201892
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#title Purification and structural studies on the complement-system control protein beta-1-H (factor H).
#cross-references MIID:83048213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano, A.; Gordon, D.L.; Burns, G.F.
#journal Biochin. Biophys. Acta (1996) 1289:305-311
#title Factor H co-purifies with thrombospondin isolated from platelet secretate.
#cross-references_MUID:96205365
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Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liver. See also PIR:NBHUHS.
                                                                                                                                                                                                                                                                                                                                                                         sidues 411-419;574-578,580-582 ##label CAR
Factor H has also been found bound to cell membranes in an unknown
manner. However, it has at least one cell attachment site motif
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Biochem. J. (1982) 20
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Three-dimensional structure of a complement control protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation; NMR structure determination, residues 927-985
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the correspondence between the two loci and the sequences indicated is unclear; factor H has been reported to have several allelic forms
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                                                                                                                                         GDB:HF2; HF
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Similarity 67.58;
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Eur. J. Immunol. (1986) 16:1351-1355
Human complement factor H: isolation of cDNA clones and partial cDNA sequence of the 38-kDa tryptic fragment containing the binding site for C3b.
                                                                                                                 Schulz, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.;
                                                                                                                                                                                                                                                                                                 Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. (1991) 21:799-802

Human complement factor H: two factor H proteins are derived from alternatively spliced transcripts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S03013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B. Biochem. J. (1988) 249:593-602
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                                                                                                   Dierich, M.P.
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                                                                                                                                                             1-33#434-449 ##label EST
only portions of this 1.8 kilobase mRNA were sequenced
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#map_position 1q32-1q32
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.;

Pearce, J.; Driscoll, P.C.; Sim, R.B.; Campbell, I.D.

#journal Biochemistry (1992) 31:3626-3634

#title Solution structure of the fifth repeat of factor H: A second example of the complement control protein module.
                                                                                                                                    #description
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Dierich, M.P.; Weiss, E.H.
#journal Eur. Immunol. (1987) 17:11485-1489
#title Human complement factor H: expression of an additional truncated gene product of 43 kDa in human liver.
#cross-references_MUID:88055295
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#accession A27877
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                                                                                                                                                                                                                                                                                                               ##cross-references GDB:129095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 226-401,'Y',403-449 ##label KRI ##cross-references GB:M12383; NID:g180472; PIDN:AAA52013.1; PID:g180473 Factor H has also been found bound to cell membranes in an unknown manner. However, it has at least one cell attachment site motif
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Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in liver. See also
a cofactor in the inactivation of C3b by serine proteinase also increases the rate of dissociation of the C3bBb complex (C3 convertase) and the (C3b)nBb complex (C5 convertase) in the alternative complement pathway complement alternate pathway
                                                                                                                                                                                                         the correspondence between the two loci and the sequences indicated is unclear; factor H has been reported to have
                                                                                                                                                                                                                                                                                                                                          GDB:HF2; HF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structural analysis of human complement protein H: homology with C4b binding protein, beta(2)-glycoprotein I, and the Ba fragment of B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDB:HF1; HF
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J. Immunol. (1986) 136:3407-3411
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Sim, R.B.; Discipio, R.G.
Biochem. J. (1982) 205:285-293
Purification and structural studies on the complement-system
control protein beta-1-H (factor H).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          form related to factor H
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21-66,52-80,85-129,
114-141,146-192,
178-205,210-251,
237-262,267-309,
294-320,325-374,
357-385,389-431,
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85-141
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                     #journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
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Local Similarity 67.48;
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                                                                                                                                                                                                                                                                                                                                           WSPAVPCLRKCYFPYLENGYNONHGRKFVOGKSIDVACHPGYALPKAQTTVTCMENGWSP 438
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Soames, C.J.; Day, A.J.; Sim, R.B.
Biochem. J. (1996) 315:523-531
Prediction from sequence comparisons of residues of factor H
                                                                                                           $65551 *type fragment factor bovine (fragment) bovine (fragment) #common_name cattle #formal_name Bos primigenius taurus #common_name cattle 19-Mar-1997 *sequence_revision 25-Apr-1997 *text_change
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#region cell attachment (R-G-D) motif\
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#binding_site carbohydrate (Asn) (c
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##residues 1-669 ##label SOA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 NGVYRPELSKYRGQDKITYECKKGFFPEIRGTDATCTRDGWVPVPRCAWKPCSYPVIKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 RVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLTPYIP
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##cross-references GB:M29010; NID:g192561; PIDN:AAA37415.1; PID:g387128
##crote translation of the nucleotide sequence is not complete
##note
                                                                                                                                                                                                                  ##molecule_type mRNA
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Similarity 58.4%;
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                                                                                                                    translation of the nucleotide sequence is not complete *superfamily complement factor H; complement factor H repeat
                                                                                                                                                                                                                                              A35068
                                                                                                                                                                                                                                                                                            B.F.; Chaplin, D.D.
J. Biol. Chem. (1990) 265:3193-3201
Identification and sequence analysis of four cfactor H-related transcripts in mouse liver.
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#title Identification and sequence analysis of four complement factor H-related transcripts in mouse liver.
#cross-references MUID:90153969
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270-325
194 ENGWSPPPKCIRIN 207
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                                                                                                                                                                                                                                                                                                                     236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG 295
                                                                                                                                                                                                                                                                              75
                                                                                                                                                                                                                                                                                                                                                             15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHKSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-303 ##label VIK
##cross-references GB:M29007; NID:g192557; PID:g309164; GB:J05259
##note translation of the nucleotide sequence is not complete
FICATION #superfamily complement factor H repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 WIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSY-WDYL 354
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Local Similarity 71.1%;
                                                                                                              RCTAQGWEPEVPCVRKCVFHYVENGDSTYWEKTYVQGQSLKVQCYNGYSLQNGQDTMTCT 193
                                                                                                                                                                                                                                                  WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYKCDNGFSPPS-GYSWDYL 133
                                              RCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCT 414
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#formal_name Mus musculus #common_name house mouse
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Pred. No. 3.28e-249;
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22; Mismatches
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Pred. No. 5.17e-251;
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                                                                                                                                                                                                                                                                                                                                                                                           14 LTAWLSTAKGEVKSCEFPOFKYGRLYFEETLRPNFPVSIGNKYSYKCDNGFSPPSGLFWD 73
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                                                                                                                                                                                                                                                                                                                                  74 YLRCTVQGWKPEVPCVRKCVFHYVENGEFAYWEKIYVQGQSLKVQCYNGYSLQNGQDTMT 133
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Dahmen, A.; Kaidoh, T.; Zipfel, P.F.; Gigli, I.
Biochem. J. (1994) 301:391-397
Cloning and characterization of a cDNA representing
                                                                                                    #formal_name Parablax neblifer #common_name barred sand
19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change
                                                                         S46199; S77894
                                                           S46199
                                                                                                                                                 probable complement regulatory plasma protein SB1 - barred
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J. Biol. Chem. (1990) 265:3193-3201
Identification and sequence analysis of four complement factor H-related transcripts in mouse liver.
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D35069; A3507
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Pred. No. 1.40e-162;
24; Mismatches 22;
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to human complement factor H. #cross-references MUID:93155112
                                                                                                         #authors
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##residues 526-532,'X',534-537;809-817,'X',819-826 ##label
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                                                                                                                                                                                                                                                                                                                                          374 HYVEYGESSYWQRR-YIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                    397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 -- PEEAT-FGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIENGNV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 NDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQVIGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references EMBL:L21703;
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Local Similarity 31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 YPGGRQVRVGCNVGY-S-GFFKLVCVEGKW-ETRGAK-CQPRSCGHPGDAQFADFHLAEG 105
                                                                                                                                                                                                                                                                                                                                                                                  ENIQDAVIVGTDKQIYNLNQKAIYACGEG-N--RGRITLTCGENGWSGDRKCT-VK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYLKPYYKENERFQYKCKQGFYYKERGDA-VCTG--SGWNPQPSCEEMTCLTPYIPNGIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDSWDVRSWERY - - - TLDDNTRYWCKRGYKRTGGVIWA - - TCGRNGWMPNPLCEVKTCSK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TP-HRIKHRIDDEIRYEC-KNGFYPATR-SPV-SKCTITG-WIPAPRCSLKPCDFPQFKH 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPAYRNLFSPGETLKVICARTSWISTPQETSVVTTCQDNGEWSIRPTCQEVRCSNRRPEH 341
                                                                                                                                                                                                                                                                                                                                                                                                                            GRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPC-LRQCIF
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#longth 1053 #molecular-weight 117597 #checksum
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                                         J. Biol. Chem. (1993) 268:2904-2908
A novel short consensus repeat-conta
                                                                                                                                                                                      #formal_name Homo sapiens #common_name man 30-Sep-1903 #sequence_revision 30-Sep-1993
                                                                                                       Skerka, C.; Kuhn, S.; Gunther, K.; Lingelbach,
                                                                                                                                                 A45222; S29609
                                                                                                                                                                                                                                   complement factor H-related protein DOWN16 precursor - human
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Pred. No. 1.28e-135;
76; Mismatches 180;
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Best Local Similarity 56.3%;
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211-265
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87-141
                       112-169
174-234
239-294
239-360
364-422
426-480
484-538
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108,186,206,310
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#residues 1-331 ##label SKE
##cross-references EMBL:X88679; NID:g30869; PID:g30870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references GDB:137201
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                                                                                                                                                                                                                                                                  ##residues
                                                                                                                                                                                                                                                                                                          ##status
                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                          de Frutos, P.G.; Dahlbaeck, B.
Biochim. Biophys. Acta (1995) 1261:285-289
CDNA structure of rabbit C4b-binding protein alpha-chain.
Preserved sequence motive in complement regulatory protein modules which bind C4b.
TOES MUID:95226458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $53711 #type complete
C4BP alpha chain precursor - rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
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#length 331 #molecular-weight 37469 #checksum 6811
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#length 597
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Pred. No. 2.32e-126;
26; Mismatches 32;
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                                                                                                                                               **ERENCE $02372

#authors Lintin, S.J.; Lewin, A.R.; Reid, K.B.M.

#journal FEBS Lett. (1988) 232:328-332

#title Derivation of the sequence of the signal peptide in human C4b-binding protein and interspecies cross-hybridisation of the C4bp cDNA sequence.

#cross-references_MUID: 46242821
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#*residues 1-597 ##label MA1
##cross-references GB:M31452; NID:g190501; PIDN:AAA36507.1; PID:g190502
                                                                ##cross-references EMBL:X07853
                                                                                       ##molecule_type mRNA
##residues 17-81 ##label LI2
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A90326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsuguchi, T.; Okamura, S.; Aso, T.; Sata, T.; Niho, Y. Biochem. Biophys. Res. Commun. (1989) 165:138-144 Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C4b-binding protein alpha chain precursor - human C4BP; proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A33568
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13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change
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                              although the sequence determined extends to residue
                                                                                                                                                                                                                                                                                                                                                            the authors translated the codon GGA for residue
               above, these authors assign Met-17 as the initiator
                                                                                                                                                                                                                                                                                                                                             Glu
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                                                                                                                                                                                                                                                                                                                                                          #authors Suzuki, K.; Nishioka, J.
#journal J. Biol. Chem. (1988) 263:17034-17039
#title Binding site for vitamin K-dependent protein S on complement
#cross-references_MUID:89034204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal #title
                                                                      #cross-references MUID:83221615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Hessing, M.; Kanters, D.; Takeya, H.; van't Veer, C.;
Hackeng, T.M.; Iwanega, S.; Bouma, B.N.

#journal FEBS Lett. (1993) 317:228-232

#title The region Ser(333)-Arg(356) of the alpha-chain of human C4b-binding protein is involved in the binding of complement C4b.

#cross-references_MUID:93146164
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#title Amino acid sequence studies of human C4b-binding protein:

N-terminal sequence analysis and alignment of the fragments produced by limited proteolysis with chymotrypsin and the peptides produced by cyanogen bromide treatment.
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#accession A24182
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##residues 381-404 ##label HES
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##residues 49-81 ##label CH1
##note this paper reports amino-terminal sequences of the
intact protein and of a number of proteolytic per
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##cross-references GB:X02865; NID:g29564; PIDN:CAA26617.1; PID:g29565
##note 92-Thr and 357-His were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
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                                                                                                          Dahlback, B.; Smith, C.A.; Muller-Eberhard, H.J. Proc. Natl. Acad. Sci. U.S.A. (1983) 80:3461-3465 Visualization of human C4b-binding protein and its complexes with vitamin K-dependent protein S and complement protein
                   annotation; electron microscopy; three-dimensional structure;
    ligand binding
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I52244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lintin, S.J.; Reid, K.B.M.
FEBS Lett. (1986) 204:77-81
Studies on the structure of the human C4b-binding
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Blochem. J. (1985) 230:133-141
Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.
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#title Genomic organization of the alpha chain of the human

C4b-binding protein gene.

#cross-references_MUID:91113199
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NT C4BP controls the classical pathway of complement activation. It
binds as a cofactor to C3b/C4b inactivator (C3bINA), which then
hydrolyzes the complement fragment C4b. It also accelerates the
degradation of the C4bC2a complex (C3 convertase) by dissociating
the complement fragment C2a.

NT C4BP occurs in plasma in two forms, both of which bind complement
fragment C4b. The prevalent higher molecular weight form contains
7 alpha chains and one beta chain, which are linked by disulfide
bonds. The beta chain binds the vitamin K-dependent plasma
protein S. A minor form lacks the beta chain. Bound protein S is
inactive as a cofactor for protein C inactivation of coagulation
factors V and VIII.
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ap_position 1q32-1q32
ntrons 48/1; 110/1; 143/2; 172/1; 236/
        176
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    -EN---GLWSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGD 230
                                                                                                                                                                                                                                                                                                                                             SRICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYR-EC-DAD-G 115
                                                                                                                                                                                                                                                                                                                                                                                                                           FCIY-KR-CRHPGELRNG--QVEIKTDLSFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVG 162
                                                                                   VENETIGVWRPSPPTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSV 278
                                                                                                                                                                      WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS 175
                                                                                                                                                                                                                                                 WSHPLPQCEIVKCKPPPDIRNGR-HSG--E-ENFYAYGFSVTYSCDPRFSLLGHASISCT 218
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#length 597 #molec
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PID:g899380
PID:g899380
PICATION #superfamily C4b-binding protein alpha chain; complement
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231 AVCTGSG-WNPQPSCEEMTCL-TPYIPNG--IYTPH-RIKH--RIDDEIRYECKNGFYPA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AVC-TGSGWNP-QPSCEEMTCLT-PYIPNGIY-T-PHRIKHRI--DDEI-RYECKNGFYP 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.7%;
Local Similarity 29.5%;
hes 132; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 --CVKKSCRNPGDLQNG--KVEVKTDFLFGSQIEFSCSEGYILIGSSTSYCEIQGKGVSW 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTDEPTTVICQKNLRWTPYQGCEALCCPEPKLNNGEIT-QH-RKS-RPANHC-VY-FYGD 393
                                                                     IHCEADGSWSPVPVCELNSCTDIPDIPNAALITSPRPRKEDVYPVGTVLRYICRPGYEPA 303
                                                                                                                                                                                                                         VVNKTVGVWSPSPPTCERIICPWPKVLHGTINSGFKHTYKYKDSVRFVCQKGFVLRGSGV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                               RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGE-IDYRECDADG--W 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKGPPPRENSEILSGSWSEQL-YSEGTQATYKCRPGY-RTLGTIVKVCKN-GEWVPSNPS
                                                                                                                                                   E-N---GLWSNEKPQCVEISCLPPRVENGD-GIYLKPVYKENERFQYKCKQGFVYKERGD 230
                                                                                                                                                                                                                                                                                                   TNDIPICEVVKC-LPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS
                                                                                                                                                                                                                                                                                                                                                                     SDPLPECVIAKCGMP-PDISNGK-HNGR-E-EEFFTYRSSVTYKCDPDFTLLGNASITCT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillarp, A.; Thern, A.; Dahlback, B. submitted to the EMBL Data Library, July 1995 Molecular cloning of rat C4b-binding protein alpha- and beta-chains: structural and functional relationships human, bovine, rabbit, mouse and rat proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S57953
S57953
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C4BP protein alpha chain precursor - rat
#formal_name Rattus norvegious #common_name Norway rat
13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #length 558
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Pred. No. 8.78e-89;
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239-294
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362 CKEVCCPEPNLNNYGSITLH--RRP----STSTHCTYISGDKISYECHSKYMFDAL-CTK 414
                                                                                                                                      302 LPHIPHALWERYDHQTQTEQQVYDIGFVLSYKCHFGYKPETDGPTTVTCQSNLEWSPYIE 361
                                                                                                                                                                                                  195
                                                                               252 -PYIPNGI---YTPH-RIKHRI-DDE-I-RYECKNGFYPATRSPVS-KC-TITGWIPAPR
                                                                                                                                                                                                                                               242 PVVKDGKITSGFGPIYTYQQSIVYACNKGFRLEGDSLIHCEADNSWNPPPPTCELNGCLG 301
                                                                                                                                                                                                                                                                                                      139 IVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS-EN---GLWSNEKPQCVEISCLP 194
                                                                                                                                                                                                                                                                                                                                                            185 -HNGGDE-DF-YTYGSSVTYSCDRDFSMLGKASISCRVENKTIGVWSPSPPSCKKVICVQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 VKTDYSFGSEIEFSCSEGYYLIGSANSYCQLQDKGVVWSDPLPQCIIAKCEPPPTISNGR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:Z31693; NID:g469117; PIDN:CAA83498.1;
PID:g469118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 TRSPVS-KCTIT-GWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 FETGTTLRYTCRPGYRISSRKNFLICDGTDNW--KYKE-FCVKKRCENPGEL-LNG-QVI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                         PRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVC-TGSGWNPQP-SCEEMTCLT 251
                                                                                                                                                                                                                                                                                                                                                                                                               VGSEFEFGAKVVYTCDEGYQLLGEID-YRECDADG--WINDIPICEVVKCLPVTELENGR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSEGTQATYKCRPGYRTLG-TIVKVCKNGE-WVPSNPSRICRKRPCGHPGDTPFGSFRLA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEEGYRLV-GEATISCWYSQWTPAAPQC 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th 14.18;
Similarity 27.98;
120; Conservative
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J. Immunol. (1994) 153:4190-4199
Bovine C4b binding protein. Molecular cloning of the alpha-
and beta-chains provides structural background for lack of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4b-binding protein alpha chain - bovine #formal_name Bos primigenius taurus #common_name cattle 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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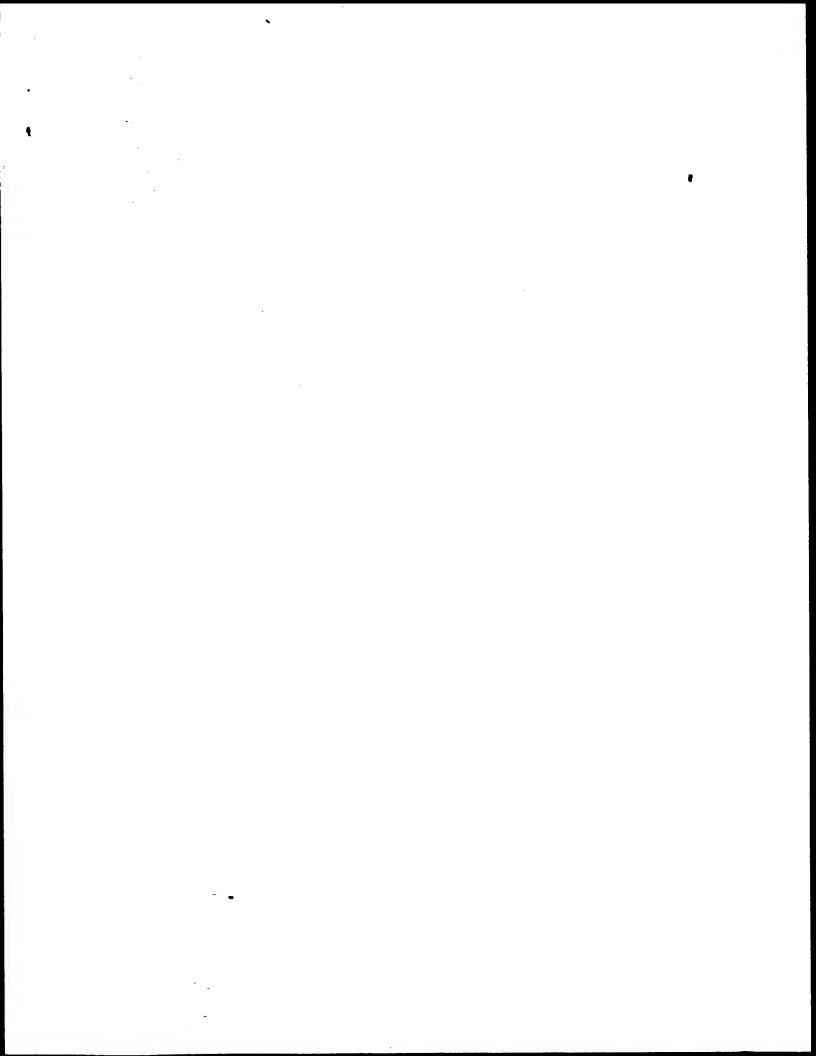
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Best Local Similarity 31.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 21-367 ##label RES 21-367 ##cross-references EMBL:U17128; NID:g595980; PID:g595982
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NCE 148306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status
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                 99 G--IEFGSTITYSCNQGYRLIGDSSATCIVSDNTVMWDNDMPLCESIPCESPPAISNGDF 156
                                                              24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                 42 FAIGTTWEYKCRPGYFRKSFIIT-CLETSKW--SDAQQFCKRKPCMNPQEPLHGSVHINT 98
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                                                                                                                                                  101;
    Wagner, L.M.; Holers, V.M.

J. Exp. Med. (1995) 181:151-159

Mouse complement regulatory protein Crry/p65 uses the specific mechanisms of both human decay-accelerating and membrane cofactor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #superfamily complement factor H repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2
                                                                                                                                                                                                                                #length 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
J. Immunol. (1990) 144:3581-3591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Mus musculus #common_name house mouse 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
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                                                                                                                                                                                                                                #checksum 1376
                                                                                                                                                                                                                                             complement factor H repeat homology complement factor H repeat homology complement factor H repeat homology
                                                                                                                                            Score 470; DB 2;
Pred. No. 6.17e-83;
72; Mismatches 111
                                                                                                                                              Mismatches 111; Indels
Length 676;
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FH03\
FH04\
FH05\
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Best Local Similarity 41.4%;
Matches 55; Conservative
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92-145
154-208
215-269
273-334
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#journal J. Biol. Chem. (1990) 265:3193-3201
#title Identification and sequence analysis of four complement factor H-related transcripts in mouse liver.
#cross-references MUID:90153969
                                                                                            413
                                                                                                                                                                           353 YLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYY 412
                                                                                                                                      134 CAEEGWSITPKCI 146
                                                                                                                                                                                                                                                                                 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-343 ##label VIK
##cross-references GB:M29008; NID:g192559; PID:g309165; GB:J05259
##note translation of the nucleotide sequence is not complete
#FICATION #superfamily complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 F-MGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPG-YTLIGTNLVECTSLGTWSNTVPT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 -ISCLPPRVENG--DGIYLKPVYKENERFQYKCKQGFVYKERGDAVC-TGSGWNPQ-PSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 CEVKSCDAIPNHLLHGRVF 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 VSGAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHC-S-EN--GLWSNEKPQCVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
                                                                                                                                                                                                                       74 RITCTESGWSPTPKCLRLCFFPFYENGNSTSSGQTHYEGDIVQVVCNQGYSLQNNQSTIT 133
                                                                                                                                                                                                                                                                                                                 14 LTSWFSTAKGEVSLCDFPKIRHGILYDEKKNEPFSSVLSGKILYYSCEYNFASPSNSFWT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 GSEFEFGAKVVYTCDEGYQLLGE--IDYRECDADG-WINDIPICEVVKCLPVTELENGRI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                       CTENGWSPPPKCV 425
                                                                                                                                                                                                                                                                          ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YS-SS-RD-SFFYGMVVTYYCHTGKNREKLFDLVGEKSIYCTSKDNQVGIWNSPPPQCIP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain complement factor H repeat homology #label FH1\
#domain complement factor H repeat homology #label FH2\
#domain complement factor H repeat homology #label FH3\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH4\
#domain complement factor H repeat homology #label FH5
#length 343 #molecular-weight 38443 #checksum 9901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G35070 #type complete
apolipoprotein H-related protein 13G1 - mouse
#formal_name Mus musculus #common_name house mouse
27-Jul-1990 #sequence_revision 31-Dec-1993 #text_change
10-Sep-1997
G35070; A35071; B35071; H35070; I35070
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Pred. No. 2.31e-77; 
29; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jun 8 21:50:30 2000; MasPar time 15.22 Seconds 856.639 Million cell updates/sec Tabular output not generated.

Title: >US-09-316-163-14
Description: (1-428) from USO9316163.pep
Perfect Score: 3371
Sequence: 1 EDCKGPPPRENSEILSGSWS.....DTYYCTENGWSPPPKCVRIK 428

Scoring table:

PAM 150 Gap 11

Searched: 83857 seqs 30454973 residues
Post-processing: Minimum March 08
Listing first 45 summaries

Database: swiss/prot38

Mean 46-246; Variance 66.763; scale 0.693

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	B B	ID	Description	Pred. No.
1	2834	84.1	1234	- ;	CFAH_MOUSE	COMPLEMENT FACTOR H PR	0.00e+00
N	2396	71.1	1231	Н	CFAH_HUMAN	COMPLEMENT FACTOR H PR	0.00e+00
ω	646	19	331	ш	CFHD_HUMAN	COMPLEMENT FACTOR H-LI	8.26e-142
4	537		597	ш	C4BP_HUMAN	C4B-BINDING PROTEIN AL	1.67e-111
տ	494	14	558	Н	C4BP_RAT	C4B-BINDING PROTEIN AL	1.09e-99
თ	474	14	610	_	C4BP_BOVIN	C4B-BINDING PROTEIN AL	3.15e-94
7	446	13	2039	ш	CR1_HUMAN	COMPLEMENT RECEPTOR TY	1.27e-86
œ	434		330	H	CFH1_HUMAN	FACTOR H	2.23e-83
9	434	12	469	ب	C4BP_MOUSE	C4B-BINDING PROTEIN PR	2.23e-83
10	431	12		ш	CFHE_HUMAN		1.44e-82
11	396	11		ш	VCP_VACCV	COMPLEMENT CONTROL PRO	3.54e-/3
12	390	11	830	ш	LEM3_HUMAN	P-SELECTIN PRECURSOR (	1.41e-/1
13	375	11.1	345	-	APOH_MOUSE	BETA-2-GLYCOPROTEIN I	
14	374	11	768	<u>بــ</u>	LEM3_RAT	P-SELECTIN PRECURSOR (	
15	367	10.9	345	<u>, , </u>	APOH_HUMAN	BETA-2-GLYCOPROTEIN I	1.79e-65
16	368		768	ب	LEM3_MOUSE	P-SELECTIN PRECURSOR (	9.73e-66
17	364	10.8	345	Н	APOH_CANFA	BETA-2-GLYCOPROTEIN I	
18	357		610	μ	LEM2_HUMAN	E-SELECTIN PRECURSOR (	
19	359		612	μ	LEM2_MOUSE	E-SELECTIN PRECURSOR (	2.31e-63
20	348	10.3	668	ч	F13B_MOUSE	COAGULATION FACTOR XII	1.80e-60
21	345		377	י	MCP_HUMAN	MEMBRANE COFACTOR PROT	
22	344	10.2	1025	ᆫ	CR2_MOUSE	COMPLEMENT RECEPTOR TY	2.01e-59
23	341	10.1	345	$\vdash$	APOH_BOVIN	BETA-2-GLYCOPROTEIN I	1.23e-36

24 335 9.9 769 1 LEM3_SHEEP P-SELECTIN PRECURSOR ( 4.52e-57 2.5 32.9 9.8 551 1 LEM2_RABIT E-SELECTIN PRECURSOR ( 1.65e-55 2.6 3.28 9.7 50.7 1 DAF_CAYPO COMPLEMENT DECAY-ACCEL 3.00e-55 2.7 32.7 9.7 661 1 F138_HUMAN COMPLEMENT DECAY-ACCEL 3.00e-55 2.7 32.7 9.7 661 1 F138_HUMAN COMPLEMENT DECAY-ACCEL 2.30e-51 3.00e-35 2.00e-35 2	/																							
9.9 769 1 LEM3_SHEEP P-SELECTIN PRECURSOR ( 9.8 551 1 LEM2_RABIT E-SELECTIN PRECURSOR ( 9.8 557 1 DAF_CAVPO  9.7 507 1 DAF_CAVPO  661 1 F13B_HUMAN COMPLEMENT DECAY-ACCEL 3 9.7 958 1 HIG_DROME LOCOMOTION-RELATED PRO 3 9.7 958 1 LEM2_PIG COMPLEMENT DECAY-ACCEL 2 9.3 381 1 DAF_HUMAN LOCOMOTION-RELATED PRO 3 9.1 1033 1 CR2_HUMAN E-SELECTIN PRECURSOR ( 9.0 611 1 LEM2_BOVIN COMPLEMENT DECAY-ACCEL 2 9.1 1033 1 CR2_HUMAN E-SELECTIN PRECURSOR ( 9.0 485 1 LEM2_BOVIN COMPLEMENT DECAY-ACCEL 2 8.7 549 1 LEM2_RAT COMPLEMENT DECAY-ACCEL 3 8.6 390 1 DAF1_MOUSE COMPLEMENT DECAY-ACCEL 3 8.1 360 1 CCPH_HSVSA COMPLEMENT CONTROL PRO 1 8.1 360 1 CCPH_HSVSA COMPLEMENT CONTROL PRO 6 8.0 646 1 LEM3_BOVIN F-SELECTIN PRECURSOR ( 8.0 646 1 LEM3_BOVIN LEMING CONTROL PRO 6 8.1 360 1 CCPH_HSVSA COMPLEMENT CONTROL PRO 6 8.1 360 1 LEM1_MOUSE COMPLIANCE COMPLEMENT CONTROL PRO 6 8.1 1 1646 1 LEM3_BOVIN LEMING CONTROL PRO 6 8.1 1 1646 1 LEM3_BOVIN LEMING CONTROL PRO 6 8.1 1 1646 1 LEM3_BOVIN LEMING CONTROL PRO 6 8.1 1 1646 1 LEM3_BOVIN LEMING CONTROL PRO 6 8.1 1 1646 1 LEM3_BOVIN LEMING CONTROL PRO 6 8.1 1 1646 1 LEM3_BOVIN LEMING CONTROL PRO 6 8.1 1 1646 1 LEMI_MOUSE L-SELECTIN PRECURSOR ( 8.1 1647 1 LEMI_PAPHA L-SELECTIN PRECURSOR ( 8.2 1647 1 LEMI_PAPHA L-SELECTIN PRECURSOR ( 8.3 1646 1 LEMI_PAPHA L-SELECTIN PRECURSOR ( 8.4 1647 1 LEMI_PAPHA L-SELECTIN PRECURSOR ( 8.5 1647 1 LEMI_P		24	25	26	27	28	29	30	31	32	ω ω	34	ω S	36	37	38	39	40	41	42	43	44	45	
769 1 LEM3_SHEEP P-SELECTIN PRECURSOR ( 1 551 1 LEM2_RABIT COMPLEMENT DECAY-ACCEL 1 6661 1 F13B_HUMAN GOMPLEMENT DECAY-ACCEL 2 381 1 DAF_HUMAN LOCOMOTION-RELATED PRO 1 APPHLYAN COMPLEMENT DECAY-ACCEL 2 1 APPHLYAN COMPLEMENT DECAY-ACCEL 2 1 APPHLYAN COMPLEMENT DECAY-ACCEL 2 1 APPHLYAN COMPLEMENT DECAY-ACCEL 340 1 LEM2_BOVIN COMPLEMENT DECAY-ACCEL 340 1 DAF1_MOUSE COMPLEMENT DECAY-ACCEL 360 1 CCPH_HSVSA COMPLEMENT DECAY-ACCEL 360 1 LEM3_BOVIN P-SELECTIN PRECURSOR ( 1019 1 LEM3_BOVIN P-SELECTIN PRECURSOR ( 1019 1 LEM1_MAGMU L-SELECTIN PRECURSOR ( 1019 1 LEM1_MAGMU L-SEL		335	329	328	327	328	323	313	309	306	304	301	294	292	291	276	274	268	255	232	226	226	225	
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SEQUENCE OF 53-445 FROM N.A.
MEDLINE; 87054207.
Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;
"Human complement factor H: isolation of cDNA clones and partial cDNA
sequence of the 38-kDa tryptic fragment containing the binding site
                                                                                                                                                                                                                                                                                           01-AUG-1988 (Rel. 08, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
COMPLEMENT FACTOR H PRECURSOR.
HEI OR HF OR CFH.
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                           MEDLINE; 88134059.

Ripoche J., Day A.J., Harris T.J.R.,

"The complete amino acid sequence of
Biochem. J. 249:593-602(1988).
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                                                                                                                                                                                                                                                                               J. MOI. BIOI. 232:268-284(1993).

-i. FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION OF FUNCTION: FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF THE C3B BY FACTOR I AND ALSO INCREASES AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.

-i. SIMILARITY: CONTAINS 20 SUSHI (SCR) REPEATS.

-i. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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"Structural analysis of human complement protein H: homology with C4b binding protein, beta 2-glycoprotein I, and the Ba fragment of B2.";
J. Immunol. 136:3407-3411(1986).
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                                                                                                                                                                                                                                                                                                                                                                                            "Solution structure of a pair magnetic resonance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barlow P.N., Norman D.G., Steinkasserer A., Horne T.J., Pearce J., Driscoll P.C., Sim B., Campbell I.D.; "Solution structure of the fifth repair of factor H: a second example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91278097.

Norman D.G., Barlow P.N., Baron M., Day A.J., Sim B., Campbell I.D.

"Three-dimensional structure of a complement control protein module
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Barlow P.N., Steinkasserer A., Norman D.G., Kieffer B.,
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                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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              ; 1HCC; 15-APR-92.
; 1HFH; 15-JUL-93.
; 1HFI; 15-JUL-93.
; 134370; -.
                                                                  S00254;
S00254;
S03013;
                                                                                                            Y00716; CAA68704.1;
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31:3626-3634(1992).
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POTENTIAL.

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"A novel short consensus repeat-containing molecule is related human complement factor H.";
J. Biol. Chem. 268:2904-2908(1993).
-i- FUNCTION: MIGHT BE INVOLVED IN COMPLEMENT REGULATION.
-i- SUBCELLULAR LOCATION: EXTRACELLULAR.
-i- SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS.
-i- SIMILARITY: STRONG, TO FACTOR H.

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  TISSUE-LIVER;
MEDLINE; 93155112.
Skerka C., Kuehn S.,
                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; (
                                                                                                     Eutheria; Primates; Catarrhini; Hominidae; Homo
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P044003;
23-0CT-1986 (Rel. 02, Created)
23-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y., "Molecular cloning of the cDNA coding for proline-rich identity of PRP as C4b-binding protein."; Biochem. Biophys. Res. Commun. 165:138-144(1989). [2]
                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                    MEDLINE; 90073699.
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PFAM; PF00084; sushi; 5.
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llarity 56.3%;
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Pred. No. 8.26e-142;
26; Mismatches 32;
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5 X SUSHI (SCR) REPEATS.
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RA Dahlback B., Smith C.A., Mueller-Eberhard H.J.;

RA "Visualization of human C4b-binding protein and its complexes with ry vitamin K-dependent protein S and complement protein C4b.";

RI Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).

RL Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).

C: -i- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT C4B. IT BINDS AS A COFACTOR TO C33/C4B INACTIVATOR

CC (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT CC ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ACOMPLERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DESCOLATING THE COMPLEMENT FRAGMENT C4B. IT CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CC SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS CC C CHAIN, A 530 KD CHOMPLEX OF 7 ALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF THE CALL NOT THE CALL NOT THE ENDING CC CALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF THE BINDING CALPHA CHAIN AND ACAD THE ENDING CC CALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF THE BINDING CALPHA CHAIN AND ACAD THE ENDING CC CALPHA CHAIN AND ACAD THE ENDING CC CALPHA CHAIN AND ADDITIONAL CHAIN AND ACAD THE ENDING CC CALPHA CHAIN AND ADDITIONAL CHAIN AND ADDITIONAL CHAIN AND ADDITIONAL CALP THE ENDING CC CALPHA CHAIN AND ADDITIONAL CHAIN AND ADDITIONAL CALP THE BINDING CC CALPHA CHAIN AND ADDITIONAL CHAIN AND ADDITIO
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"Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and alignment of the fragments produced by limited proteolysis with chymotrypsin and the peptides produced by cyanogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chung L.P., Bentley D.R., Reid K.B.M.; "Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system."; Biochem. J. 230:133-141(1985).
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Lintin S.J., Lewin A.R., Reid K.B.M.;
Tintin S.J., Lewin A.R., Reid K.B.M.;
"Derivation of the sequence of the signal peptide in human
"Derivation protein and interspecies cross-hybridisation of the C4bp
CDNA segmence.":
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EMBL; M31452;
EMBL; M62486;
EMBL; M62475;
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                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way the content is in the content is 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITE FOR C4B AT THE END.
TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
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116 WINDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS
             163 WSHPLPQCEIVKCKPPPDIRNGR-HSG--E-ENFYAYGFSVTYSCDPRFSLLGHASISCT
                                                                          49 NC-GPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNT 106
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M62481 AAA36506.1;
M62482 AAA36506.1;
M62484 AAA36506.1;
M62484 AAA36506.1;
M67853 CAA30701.1;
X07853 CAA30701.1;
X04284 CAB51244.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M62476;
M62477;
M62478;
M62479;
                              SRICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYR-EC-DAD-G
                                             FCIY-KR-CRHPGELRNG--QVEIKTDLSFGSQIEFSCSEGFFLIGSTTSRCEVQDRGVG
                                                            DCKGPPPREN-SEILSGSWSEQLYSEGTQATYKCRPGY-RTLGTIVKVCK-NGEWVPSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P10998; 1VVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X02865; CAA26617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X04296; CAA27839
                                                                                            138;
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  pathway;
                                                                                                                         597 AA;
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50
81
113
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                                                                                           Conservative
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AAA36506.1;
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/FTId=VAR_001977.
Y -> H
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85; 1
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Y SIMILARITY.
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                                                                                             Mismatches
                                                                                                   DB 1; Le
L.67e-111;
                                                                                                                                                                                       HTIW)
                                                                                                                                                                                       BETA CHAIN)
BETA CHAIN)
                                                                                                           Length 597
                                                                                                                                                                                       (POTENTIAL).
                                                                                             45;
                                                                                             Gaps
                  218
                                                               58
                                115
                                                162
                                                                                              40;
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밁 δÃ 멍 γQ 문 δÃ 당 Š 밁

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A Hillary A., Wiklund H., Thern A., Dahlback B.;

RT "Molecular cloning of rat C4b binding protein alpha- and beta-chains: molecular cloning of rat C4b binding protein alpha- and beta-chains: molecular cloning of rat C4b binding protein alpha- and beta-chains: molecular cloning of rat C4b binding protein alpha- and beta-chains: molecular cloning of rat C4b binding protein. Table controls of chassical partway of complement cap.

CC ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

CC ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

CC ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

CC (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT

CC ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3

CC CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C4B. ALPHA

CC CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S

CC SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS.

CC -!- SUBULLARITY: CONTAINS 8 SUSHII (SCR) REPEATS.

CC -!- SIMILARITY: CONTAINS 8 SUSHII (SCR) REPEATS.
                                         REPEAT
REPEAT
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REPEAT
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C4BP_RAT STANDARD; PRT; 558 AA Q65314; Q65314; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-7UL-1998 (Rel. 36, Last annotation updat C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR. C4BPA.
                                                                                                                 DOMAIN
                                                                                                                                                                                                                         EMBL; Z50051; CAA90391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER; MEDLINE; 97166082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                      PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-GFTTPSQSYWDYLRCTVNG-WEPEVP-CLRQCIFHYVEYGESSYWQRR-YIEGQSAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EISFSCHETSRFSAI-CQGDGTWSPRTPSCGDICNFP-PKIAHGHYKQSSSYSFFKEEII
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                                                                                                                                                                                                      P10998; 1VVC
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                                                                                                                                                                  pathway;
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               C4B-BINDING PROTE
8 X SUSHI (SCR) F
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SUSHI 2.
SUSHI 3.
SUSHI 4.
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Best Local
                       C4BP_BOVIN
Q28065;
01-NOV-1997
01-NOV-1997
         C4B-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 -- CVKKSCRNPGDLQNG--KVEVKTDFLFGSQIEFSCSEGYILIGSSTSYCEIQGKGVSW 127
                                                                                                                                                                        CHSGYSLPNGQDTYYCTENGWSPP-PKC
                                                                                                                                                                                                                                                                            VSYTCQNDIMLT-ATCKSDGTWHPRTPSCHQSCDFPPAIAHGRYTKSSSYYVRTQVT-YE
                                                                                                                                                                                                                                                                                                                                                                                        CEEGYRLV-GEATISCWYSQWTPAAPQC 443
                                                                                                                                                                                                                                         -GFTTPSQSYWDYLRCTVNG-WEPEVP-CLRQCIFH-YVEYGESSYWQRRYIEGQSAKVQ
                                                                                                                                                                                                                                                                                                                TRSPVS-KCTIT-GWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDN
                                                                                                                                                                                                                                                                                                                                                   TRQPMTVICQKDLSWSMLRGCKEICCPVPDPKSVRVI-QHEK-AH-P-DNDCTY-FFGDE
                                                                                                                                                                                                                                                                                                                                                                                                                              IHCEADGSWSPVPVCELNSCTDIPDIPNAALITSPRPRKEDVYPVGTVLRYICRPGYEPA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDPLPECVIAKCGMP-PDISNGK-HNGR-E-EEFFTYRSSVTYKCDPDFTLLGNASITCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGE-IDYRECDADG--W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
(Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation updat
PROTEIN ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.7%;
llarity 29.5%;
Conservative
                                                                                                  STANDARD;
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Pred. No. 1.09e-99;
89; Mismatches 18;
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SUSHI 7.
SUSHI 7.
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BY SIMILARITY.
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INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
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THE FEFFER AND SOCIOLOGICAL STREET FOR SOCIOLOGICAL ST

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Eukaryota;
Eutheria; (
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DISULFID
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DISULFID
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                                                                DISULFID DISULFID
                                                                                                                                                                                                                                                              CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C4BPA
                        CARBOHYD
CARBOHYD
                                                                                DISULFID DISULFID
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REPEAT
                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovinae; Bos.
                 CARBOHYD
                                         DISULFID
                                                DISULFID
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         CARBOHYD
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SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                PF00084; sushi;
                                                                                                                                                                                                                                                                                                       Z31693; CAA83498.1;
P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95015909.
                                                                                                                                                                                                                                                                                                                                       requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s (Bovine).
; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae;
                 2366
2367
2402
429
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514
514
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221
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 A
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2412
425
471
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  68886
  MM
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8 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
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SUSHI 6.
SUSHI 7.
                                                                                                                                                                                                                                                                               Glycoprotein; Repeat; Sushi; BY SIMILARITY.
                                                         INTERCHAIN
INTERCHAIN
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                                         BETA CHAIN)
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Best Local :
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                                                                                                                                                                                    SEQUENCE;
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P17927;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B
                                                                                                                                                                                                                             "Identification of distinct C3b and C4b human C3b/C4b receptor (CR1, CD35) by de J. Exp. Med. 168:1699-1717(1988).
"Identification of a partial cDNA clone complement fragments C3b/C4b."; Proc. Natl. Acad. Sci. U.S.A. 82:7711-77
                                                                                                repeating domains that are composed of characteristics of C3/C4 binding protei J. Exp. Med. 165:1095-1112(1987).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 89035992.
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                         ANTIGEN).
CR1 OR C3BR
                                        MEDLINE; 86067975.
Wong W.W., Klickstein L.B.,
                                                                                                                                                        Fearon D.
                                                                                                                                                                     Klickstein L.B.,
                                                                                                                                                                                                                                                                          Fearon D.T.;
                                                                                                                                                                                                                                                                                      Klickstein L.B.,
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                      SEQUENCE
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                                                                                                                                           Human C3b/C4b receptor (CR1). Demonstration of long homologous
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mes 120; Conser
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                               Craniata; Ve
i; Hominidae;
 82:7711-7715(1985)
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                                          J.A.,
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deletion mutagenesis.
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                            weis J.H., Fearon D.T.;
for the human receptor for
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EMBL; M11569; AAA52297.1; -.
EMBL; M11617; AAA52298.1; -.
EMBL; M11618; AAA52299.1; -.
EMBL; V00816; CAA68755.1; -.
EMBL; X05309; CAA28933.1; -.
EMBL; X05309; CAA28933.1; -.
PIR; A24748; A24748.
PIR; B24748; B24748.
PIR; B24748; B24748.
PIR; C24748; C24748.
PIR; C3843; S03843.
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-!- SUBGUNIT: MONOMER.
-!- SUBGURIT: MONOMER.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- POLYMORPHISM: CR1 IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTEM.
-!- MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A CONTALNED A SITE DETERMINAL TWO SRCS OF LHR-A CONTALNED A SITE DETERMINAL TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINAL TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3 SPECIFICITY.
-!- MISCELLANEOUS: THIS IS THE SEQUENCE OF THE F ALLOTYPE OF CR1.
-!- SIMILARITY: CONTALNS 30 SUSHI (SCR) REPEATS.
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                                                                                                                                              DOMAIN
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              SUSHI AA.
SUSHI BA.
SUSHI CA.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PYRROLLIONE CARBOXYLIC ACID (POTENTIAL).
7 X SUSHI (SCR) REPEATS, LONG HOMOLOGOUS
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                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36).
                                                          MEDLINE; 91201892.
Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss E.H.;
Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss E.H.;
Cloning of the 1.4-kb mRNA species of human complement factor H
reveals a novel member of the short consensus repeat family related
to the carboxy terminal of the classical 150-kDa molecule.";
J. Immunol. 146:3190-3196(1991).
                                                                                                                                                                       Homo sapiens (Human).
Fikaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                      Q03591;
01-JUN-1994
                                                                                                                                                                                                                                                                              CFH1_HUMAN
                      SEQUENCE OF 4-330 FROM N.A. MEDLINE; 91268081.
                                                                                                                                                                    Eutheria; Primates;
                                                                                                                                 TISSUE-LIVER
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
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"Molecular cloning of a human serum protein structurally related to
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                                                                                                                                                                      Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 446;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                      Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 108; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B2FD29B6AD3C5EB7 CRC64;
                                                                                                                                                                                                                                                                                  330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
..27e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                               244
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RAY RAY OCC OCC RAY RAY
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement factor H.";
J. Biol. Chem. 266:12015-12020(1991).
-!- FUNCTION: MIGHT BE INVOLVED IN COMPLEMENT REGULATION.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                              P08607;
01-AUG-1988 (Rel. 0
01-FEB-1994 (Rel. 2
01-NOV-1997 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M65292; AAA35946.1; -. EMBL; M65293; AAA35947.1; -. EMBL; X56209; CAA39666.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: LIVER.
-!- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
-!- SIMILARITY: STRONG, TO FACTOR H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P08603; 1HFI.
MIM; 134371; -.
PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A40455; A40455.
PIR; S14604; S14604.
                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                          C4BPA OR C4BP
                                                                                                   C4B-BINDING PROTEIN PRECURSOR (C4BP).
                                                                                                                                                             C4BP_MOUSE
                                                                             Mus musculus (Mouse).
                                                        Eutheria;
                                                                   Eukaryota;
          Kristensen
                     MEDLINE; 88024997
                                                                                                                                                                                                         367 CLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKC 424
                                                                                                                                                                                                                                                      307
                                SEQUENCE FROM N.A.
CDNA structure of murine C4b-binding
                                                                                                                                                                                                                              83 CLRLCFFPFVENGHSESSGQTHLEGDTVQIICNTGYRLQNNENNISCVERGWSTPPKC
                                                                                                                                                                                                                                                                          23 CDFPKINHGILYDEEKYKPFSQVPTGEVFYYSCEYNFVSPSKSFWTRITCTEEGWSPTPK 82
                                                                                                                                                                                                                                                                                                               local
                                                                                                                                                                                                                                                      CDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                Similarity
                                                      Rodentia;
                                                                                                                                                                                                                                                                                                                                                  330 AA;
          T., Ogata R.T.,
                                                                                                                                                                                                                                                                                                                                                                                   175
                                                                                                                                                                                                                                                                                                                                                                                                                               146
207
265
126
194
157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
22
22
86
                                                                                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                             STANDARD;
                                                                                                              08, Created)
28, Last sequence update)
35, Last annotation update)
                                                                                                                                                                                                                                                                                                                12.9%;
                                                                                                                                                                                                                                                                                                                                                                                   175
                                                                                                                                                                                                                                                                                                                                                                                                          159
                                                                                                                                                                                                                                                                                                                                                                                                                               330
328
84
141
202
203
263
328
126
194
                                                                                                                                                                                                                                                                                                                                                  71
37661 MW;
                                                        Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sushi;
            Chung L.P.,
                                                                                                                                                                                                                                                                                                               Score 434; DB 1;
Pred. No. 2.23e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEMENT FACTOR H-LIKE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUSHI
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                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_001981
                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_001980
                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                         /FTId=VAR_001982
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8DC0D3F92A85E035 CRC64;
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                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                               469
 protein,
             Reid K.B.M.,
                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                           Length 330;
   regulatory
                                                                                                                                                                                                                                                                                                        Indels
              Tack B.F.;
                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                        0
    component
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CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
117 TNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSE 176
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                       CARBOHYL
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                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the serum complement system.";
Blochemistry 26:4668-4674(1987).

-i- FUNCTION: C48P CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.

-i- SUBUNIT: HOMOHEPTAMER; NOT COVALENTLY LINKED. MOUSE LACKS THE
                        170 SNPFPECVIVKCGPPPDISNGK-HSGT-E-DF-YPYNHGISYTCDPGFRLVGSPFIGCTV
                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M17122; AAA37312.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement pathway;
                                                                                                                                 58 C-GPPP-AIPNALPASDVNRTDFESHTTLKYECLPGYGRGISRMMYYCKPSGEWEISV-S 114
                                                                                                                ω
                                                                                                                                                                                 Match 12.9%;
Local Similarity 31.0%;
                                                   RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYR-ECDADG--W 116
                                                                            --CAKKHCRNPGYLDNG-Y-VN-GETITFGSQIEFSCQEGFILVGSSTSSCEVRGKGVAW 169
                                                                                                       CKGPPPRENSEILSGSWSEQL-YSEGTQATYKCRPGY-RTLGTIVKVCK-NGEWVPSNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO C4BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:88229; C4BP.
                                                                                                                                                                    118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P10998; 1VVC.
                                                                                                                                                                                                                         469
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                   1160
2176
223
240
289
343
353
355
413
413
275
2275
2275
2366
381
                                                                                                                                                                                                                       51551 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                      C4B-BINDING PROTEIN.
6 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 5.
SUSHI 6.
BY SIMILARITY.
                                                                                                                                                                             Score 434; DB 1;
Pred. No. 2.23e-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Repeat; Sushi; Signal.
                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                    41E137CB8D8C6321 CRC64;
                                                                                                                                                                Mismatches 139;
                                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                        Length 469;
                                                                                                                                                             Indels 41;
                                                                                                                                                              Gaps
                                                                                                         59
                                                                                                                                                              36;
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RESULT TO A COLOR RESULT TO A 
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                                                                                                                        Matches
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Best Local
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CARBOHYD
                                                                                                                                                                                                                                                                                                               DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                     SEQUENCE
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PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skerka C., Timman C., Horstmann R.D., Zipfel P.E.; "Two additional human serum proteins structurally related complement factor H. Evidence for a family of factor H-rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; x64877; CAA46096.1; PIR; S24564; S24564.
                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last anotation update)
COMPLEMENT FACTOR H-LIKE PROTEIN DDESK59 PREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes.";
307 CDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLULAR LOCATION: EXTRACELLULAR.
-:- SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS
-:- SIMILARITY: STRONG, TO FACTOR H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92251200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P36980;
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFHE_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·!- FUNCTION:
                                                23 CDFPKINHGILYDEEKYKPFSQVPTGEVFYYSCEYNFVSPSKSFWTRITCAEEGWSPTPK 82
                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunol. 148:3313-3318(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 S--QSISCSESGTWYPEVPRC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 SYMDYLRCTVNG-WEPEVP-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 KCTITGWI-PAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 VCTGSG-WNPQPSCEEMTC-LTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 VNKTVPVWSSSPPTCEKIICSQPNILHGVIVSGYKATYTHRDSVRLACLNGTVLRGRHVI 285
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                                                                                                                     Similarity
50; Conser
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                                                                                                                                                                                                                            270 AA;
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                                                                                                                                                                                                                               30651 MW;
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                                                                                                            Score 431; DB 1;
Pred. No. 1.44e-82;
22; Mismatches 46
                                                                                                                                                                                                                                                                       COMPLEMENT FACTOR H-LIKE PROTEIN DDESK59.
4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                             Length 270;
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367

CLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKC

424 140

CLRICFFPFVENGHSESSGQTHLEGDTVQIICNTGYRLQNNENNISCVERGWSTPPKC

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RESULT
                                   J. MOI. BIO1. 272:253-265(1997).

J. MOI. BIO1. 272:253-265(1997).

IN FUNCTION: SERVES TO PROTECT THE VIRUS AGAIN:
INHIBITING BOTH CLASSICAL AND ALTERNATIVE P.
ACTIVATION. BINDS C3B AND C4B.

IS SIMILARITY: BELONGS TO THE SUPERFAMILY OF T.
COMPLEMENT ACTIVATION (RCA).

IC SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
COMPLEMENT CONTROL PROTEIN PRECURSOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P10998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kotwal G.J., Moss B.;
"Analysis of a large cluster of nonessential genes deleted
vaccinia virus terminal transposition mutant.";
Virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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"Vaccinia virus encodes
to complement control p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                   antibody-dependent complement-enhanced and contributes to virulence.";
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-COPENHAGEN;
MEDLINE; 91021027.
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                                                                                                                                                  Barlow
                                                                                                                                                            Wiles A.P., Shaw G.,
                                                                                                                                                                                   STRUCTURE BY NMR
                                                                                                                                                                                                                                            "Vaccinia virus complement-control protein prevents
                                                                                                                                                                                                                                                                             FUNCTION.
                                                                                                                                                                                                                                                                                                  Paoletti E.;
Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                       Goebel S.J., Johnson
                                                                                                                                                                                                                                                                                                                                   STRAIN-COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                       "The complete DNA sequence of 
Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                           Paoletti E.
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                         MEDLINE;
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European
                                                                                                                         ement activation.
                                                                                                                                      studies of a viral protein
                                                                                                                                                                                                         Natl. Acad.
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                                                                                                                                                  P.N.;
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Bioinformatics Institute.
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stage; Poxviridae;
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(VCP) (SECRETORY PROTEIN
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                                                                                                                                                                                                                                 neutralization
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                                                                                          AGAINST COMPLEMENT ATTACK BY FIVE PATHWAYS OF COMPLEMENT
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REPEAT
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EMBL; M22812; AAA69605.1;
EMBL; M35027; AAA47997.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
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                               "Cloning of GMP-140, a granule me
endothelium: sequence similarity
adhesion and inflammation.";
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Cr
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                       LEM3_HUMAN
                                                                 MEDLINE; 89168432.
Johnston G.I., Cook R.G.,
"Cloning of GMP-140, a gr:
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC
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81; Conse
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AAA69605.1;
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35.2%;
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i; 3D-structure.
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                                                             McEver R.P.;
anule membrane protein of
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37; 1
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Pred. No. 3.54e-73;
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                                                    proteins
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PRINTS; PR00343; SELECTIN.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS00615; C_TYPE_LECTIN_2;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PFAM; PF00008; EGF; 1.
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Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
"The P-selectin gene is highly polymorphic: reduced frequency of the
Pro715 allele carriers in patients with myocardial infarction.";
Hum. Mol. Genet. 7:1277-1284(1998)
-i- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARRAGES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LICAND RECOGNIZED IS STAUYL-LEWIS X.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL.
AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                              THE CELL SURFACE.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 9 SUSHI (SCR) REPEATS.

DATABASE: NAME-PROW; NOTE-CD guide CD62P entry;

ACCOUNTS OF THE CONTAINS 1 C
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PF00059;
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M60217; AAA35910.1;
M60218; AAA35910.1;
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24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTP-FGSFR-L 80
                                        Similarity
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                               Score 390; DB 1;
Pred. No. 1.41e-71;
87; Mismatches 191
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C-TYPE LECTIN (SHORT FORM)
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BY SIMILARITY
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at; Polymorphism; 3D-structure.
                                                               FBC407BA2579F6EB CRC64;
                               Mismatches 191;
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Q1-APR-1993 (Rel. 25, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-APR-1999 (Rel. 38, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) (B2GPI).
                                                      Kristensen T.;

"Structure of the human beta-2-glycoprotein I gene.";

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

"I FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.

"I TISSUE SPECIFICITY: PLASMA."

"I SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Mus musculus (Mouse).
Piikarvota; Metazoa; Chordata; Craniata; Vertebrata;
Murinae; Murinae;
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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EMBL; Y11356; CAA72190
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        LEM3_RAT STANDARD; PRT; 768 AA.
p98106;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
p-SELECTIN PRECURSOR (GRAULLE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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                                                                                                                                                                                              GYVNYPAKPVLLYKDKATFGCHETYKLDGPEEAECTKTGTWSFLPTCRE-SCKLPVKKAT
                                                                                                                                                                                                                                                                 VGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADG-WTNDIPICEVVKCLPVTELENGRIV
                                                                                                                                                   VLYQGMRVK 281
                                                                                                                                                                                                                                                                                                                 YSEGTQATYKCRPGYRTLGTIVK-VCK-NGEWVPSNPSRICRKRPCGHPGDTPFGSFRLA
                                                                                                                                                                         GDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTGSG-WNPQPSCEEMTCLTPYIPNG
                                                                                                                                                                                                                     SGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISC-LPPRVEN
                                                                                                                                                                                                                                            DYRPSAGNNSLYQDTVVFKCLPHFAMIGNDTVMCTEQGNWTRL-PECLEVKCPFPPRPEN
                                                                                                                                                                                                                                                                                         --S-FEYPKNISFACNPGF-FLNGTSSSKCTEEGKWSPDIPACARITCPPPPVPKFALLK 154
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MODIFIED-SUSHI.
BY SIMILARITY.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                 Indels 15;
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AND AUGDAMPACH J.A., Oliver M.G., Anderson D.C., Manning A.M.;

RT "Cloning, sequence comparison and in vivo expression of the gene
RT encoding rat p-selectin.";

RL Gene 145.251-255(1994).

C -!- FUNCTION: CA(2+) - DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
C TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
C INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LUKCCYTES. THE LIGAND RECOGNIZED IS SIALLL-LEWIS X.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC LUNG, BRAIN, LIVER, HEART, KIDNEY, THYMUS, SMALL INTESTINE.
C -!- SIMILARITY: CONTAINS 1 EAGT-LIKE DOMAIN.

C -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; RAT P-LECTIN LACKS THE

HUMAN SUSHI-2 EQUIVALENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0343; SELECTIN.
PROSITE; PS01022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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C-TYPE LECTIN (SHORT FORM).
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                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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Best Local
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                                                                  Eukaryota;
           TISSUE=LIVER
                         SEQUENCE FROM N.A.
                                                     Eutheria; Primates;
                                                                            Homo sapiens
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APOH_HUMAN STANDARD; PRT; 345 AA.
P02749;
21-JUL-1986 (Rel. 01, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
BETA-2-GLYCOPROTEIN I PRECURSOR (AFOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C. BINDING PROTEIN) (APC INHIBITOR) (B2GPI).
                                                                                                                                                                                                                                                                                                                                                                                                  368 -LRQCI-FHY-VEYG-ESSY-WQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENG-WSPP
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                  Chordata; Craniata; Vertebrata; Mammalia;
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87;
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Pred. No. 2
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26FD7E8A5F3F1316 CRC64;
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Day J.K., Warner P., Arnaud P.;
Werner P., Arnaud P.;
"Molecular cloning and sequence analysis of
apolipoprotein H (beta 2-glycoprotein I).";
apolipoprotein H (beta 2-glycoprotein I).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steinkasserer A., Estaller C., Weiss E., "Complete nucleotide and deduced amino ac glycoprotein I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence and expression of the human apolipoprotein H (beta 2-glycoprotein I)."; Gene 108:293-298(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kristensen T., Schousboe I., Boel E., Mulvihill E.M., Hansen Moller K.B., Hundahl Moller N.P., Sottrup-Jensen L.; "Molecular cloning and mammalian expression of human beta 2-glycoprotein I cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
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                                                                                                            "Qualitative analysis of the car
apolipoprotein H.";
J. Protein Cho-
                                                                                                                                                                                                                                                Steinkkasserer A., Campbell I.D., Sim
                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 20-345, CARBOHYDRATE-BINDING SITES, MEDLINE; 84222015.
                                                                                                                                                                                                                                                                                                                                                                                                                               Kristensen T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) CDNA cloning and inter-species differences of beta 2-GPI in alternation of anticardiolipin binding."; Int. Immunol. 3:1217-1221(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsuura E., Igarashi
Yasuda T., Koike T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
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                                                                                                                                                                                                                                                                           DISULFIDE BONDS IN C-TERMINAL DOMAIN MEDLINE; 93050249.
                                                                                                                                                                                                                                                                                                            Lozier J., Takahashi N., Putham r.m.;
"Complete amino acid sequence of human plasma beta 2-glycoprotein I.";
Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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Bouma B., de Groot P.G., van Den Elsen J.M.H., Ravelli R.B.G., Schouten A., Simmelink M.J.A., Derksen R.H.W.M., Kroon J., Gros P., "Adhesion mechanism of human beta(2)-glycoprotein I to phospholipids based on its crystal structure.";
                                                                                                                                                                                                                        domain
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                                                       MEDLINE; 99437994
                                                                                                                                                                                ANALYSIS OF CARBOHYDRATES
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                                                                                                                                                                                                        *Activity, disulphide mapping and structural modelling of the fifth domain of human beta 2-glycoprotein I."; PBS Lett. 313:193-197(1992).
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J.R., O'Hara P.J.,
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Steinkasserer A., Doerner C., Wuerzner R., Sim R.B.; "Human beta 2-glycoprotein I: molecular analysis of DNA and amino acid polymorphism.";
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Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.;

Sanghera D.K., Wagenknecht D.R., McIntyre J.A., Kamboh M.I.;

"Identification of structural mutations in the fifth domain of a structural mutations in the fifth domain of a structural mutations."
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"Molecular basis of the apolipoprotein H (beta 2-glycoprotein polymorphism.";
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X53595; CAA37664.1; -...
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V -> L (IN 23% OF THE POPULATION).
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C -> G (LOSS OF PHOSPHATIDYLSERINE-BINDING).
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W -> S (IN APOH*3W; LOSS OF PHOSPHATIDYLSERINE-BINDING).
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MW; 63101704F8DDFE3F CRC64;
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Pred. No. 1.79e-65;
54; Mismatches 106; Indels 21;
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MPsrch\_pp Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Thu Jun 8 21:51:06 2000; MasPar time 36.70 Seconds 808.665 Million cell updates/sec

Run on:

Tabular output not generated.

Description: Perfect Score: Scoring table: Sequence: PAM 150 Gap 11 >US-09-316-163-14 (1-428) from US09316163.pep 3371 1 EDCKGPPPRENSEILSGSWS......DTYYCTENGWSPPPKCVRIK 428

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% LisyIng first 45 summaries

Database:

ptrembl/2 1:sp\_Airchea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 45.569; Variance 69.358; scale 0.657

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2395	71.0	449	4	Q14570	,-	0
2	1720	51.0	669	თ	Q28085	CCP MODULES 3-12, WITH	0
ω	1136	33.7	452	11	Q61407	COMPLEMENT FACTOR H-RE	ω
4	1129	33.5	303	1	Q61405	COMPLEMENT FACTOR H-RE	N
ъ	790	23.4	808	11	Q61408	COMPLEMENT FACTOR H-RE	₹ 4.80e-173
σ	683	20.3	1053	13	Q91275	COMPLEMENT REGULATORY	2.44e-144
7	520	15.4	533	11	008569	ACROSOMAL MATRIX COMPO	w
8	480	14.2	522	σ	Q28769	COMPLEMENT RECEPTOR (F	F 7.77e-91
9	471	14.0	559	11	Q63135	COMPLEMENT REGULATORY	1.66e-8
10	470	13.9	657	4	Q14006	COMPLEMENT H FACTOR (F	3.02e-8
11	470	13.9	679	11	Q99254	COMPLEMENT RECEPTOR TY	3.02e-8
12	456	13.5	1911	σ	029528	COMPLEMENT RECEPTOR 1	1.256
13	448	13.3	331	4	Q92496	COMPLEMENT FACTOR H-RE	Ľ
14	447	13.3	343	11	Q61406	COMPLEMENT FACTOR H-RE	2.60e
15	449	13.3	661	σ	Q29531	COMPLEMENT RECEPTOR 1	7.94e-83
16	449		2014	σ	Q29530	COMPLEMENT RECEPTOR 1	7.94e-83
17	446	13.2	2039	4	Q16745	COMPLEMENT RECEPTOR 1	. 4.70e-82
18	446		2489	4	Q16744	COMPLEMENT RECEPTOR 1	. 4.70e-82
19	427	12.7	522	σ	Q28797	UNKNOWN PROTEIN (FRAGM	ω
20	426	12.6	243	4	Q14310	FER-2 PRECURSOR.	6.37e-77

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CD46.  MEMBRANE COFACTOR P COMPLEMENT RECEPTOR	MEMBRANE COFACTOR	COFA	DJ780M13.1.1 (SE	MEMBRANE COFACTOR	MEMBRANE COFACTOR	DJ780M13.1.2 (SEI	B19L.	D15L.	D12L PROTEIN.	HOMOLOG OF VACCINIA	FURROWED.	41KBP FRAGMENT FROM	ORF 4.	512 ANTIGEN (FRAGMENT)	ORF 04.	512 ANTIGEN PRECURSOR	CELL ADHESION MOLECULE	ZONA PELLUCIDA 3 F	COMPLEMENT RECEPTOR	COMPLEMENT BINDING	COSMID T07H6.
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ch 71.0%; Score 2395; DB 4; Length 449;	. 1 18 POTENTIAL. 19 449 POTENTIAL. DE 449 AA; 51033 MW; 61231E1B CRC32;	P10998; IVVC: PF00084; sushi; 7.	CAA82763	M12383; AAA52013.1; U56979; AAB01987.1;	CAA30403.1;	993),	_	ed (APR-1996) to the EMBL/GenBank/DDBJ databases.	WILLIAMS S.A.;	TE OF 1-19 FROM N.A.	3407-3411(1986).	beta 2-glycoprotein I, and the Ba fragment of B2.	of himse complement protein H: homology with	86169701.			Biochem. J. 249:593-602(1988).		J., HARRIS T.J.R., SIM R.B.;		E FROM N.A.	a; Primates; Cacarrithr, homenrae, nome.	Metazoa; Chordata; Craniata; Ver	ns (Human).		FACTOR H PRECURSOR.	(TrembLrel.	(TrEMBLrel. 01, Created)	35:	DREITHTNARY: PRT: 449 AA.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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TISSUE=LIVER;
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136 NGRIVSGAAGPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPP 195
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                     63 NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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                                                                                       3 GSPHLAEGNQFEYGAKVVYTCDEGYQMVGEMNFRECDTNGWTNDIPICEVVKCLPVTEPE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                             GSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWINDIPICEVVKCLPVTELE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSPAVPCLRKCYFPYLENGYNQNYGRKFVQGKSIDVACHPGYALPKAQTTVTCMENGWSP 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCTLKPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYYCDEHFETPSGSYWDHIHCTQDG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPRCIRV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNEKPQCVEISCLPPRVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                 PF00084; sushi; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSR
                                                                                                                                                                                                                                                                                                                                                                                                          Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                        669 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                          669
75683 MW; FAF0D174 CRC32;
                                                                                                                        Score 1720; DB 6; L
Pred. No. 0.00e+00;
64; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.00e+00; 64; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669
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                                                                                                                                                      Length 669;
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Q61405
Q61405;
PRELIMINARY;
Q61405;
Q01405:
01-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-NOV-1999 (TREMBLREL. 12, Last annotation update)
COMPLEMENT FACTOR H-RELATED PROTEIN.

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q61407 PRELIMINARY; PRT; 452 AA.
Q61407;
Q61407;
Q61407;
Q1-NOV-1996 (TIEMBLIFEL 01, Created)
Q1-NOV-1996 (TIEMBLIFEL 12, Last sequence update)
Q1-NOV-1999 (TIEMBLIFEL 12, Last annotation update)
COMPLEMENT FACTOR H-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M29010; AAA37415.1; -. HSSP; P08603; 1HFI. PFAM; PF00084; sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIK D.P., MUNOZ-CANOVES P., CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
VIK D.P., MUNOZ-CANOVES P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    415
                                                                                                                                                                                                                                                                                                                                                                                                                         194 ENGWSPPPKCIRIK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 WIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSY-WDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 VEYGESSYWQRRYIEGQSAKVQCHSGYSLFNGQDTYYCTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 RLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLRQCIFHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYRCDNGFSPPS-GYSWDYL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHRSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 RLYY--SYRGYFFARVNQQFVYSCDHHFVPPSQRSWDHLACTAEGWSPEEPCLRQCIFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                    ENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCTAQGWEPEVPCVRKCVFHYVENGDSAYWEKIYVQGQSLKVQCYNGYSLQNGQDIMTCT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGHNQHREEKYLQGETVRVHCYEGYSLQNDQNTMTCTESGWSPPPRCIRVK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAPRCSLKPCDFPQFKHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 33.7%;
Similarity 71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 084; sushi; 7.
452 AA; 51602 MW; 45C0BF61 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1136; DB 11;
Pred. No. 3.25e-267;
22; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOZONO H., MARTIN L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOZONO H., MARTIN L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 452;
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Matches
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                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q61408;
Q61408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and sequence analysis of four complement factor H-related transcripts in mouse liver.";
J. Biol. Chem. 265:3193-3201(1990).
EMBL; M29007; AAA37413.1; ...
HSSP; P10998; 1vvC.
PFAM; PF00084; sushi; 4.
SEQUENCE 303 AA; 34498 MW; 39350FD1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 90153969.
VIK D.P., MUNOZ-CANOVES P., KOZONO H., MARTIN L.G., TACK B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TIEMBLIE1. 01, Created)
01-NOV-1996 (TIEMBLIE1. 01, Last sequence update)
01-NOV-1999 (TIEMBLIE1. 12, Last annotation update)
COMPLEMENT FACTOR H-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                    "Identification and sequence analysis of four complement factor related transcripts in mouse liver.";
J. Biol. Chem. 265:3193-3201(1990).
                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 90153969.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                   CHAPLIN D.D.;
                                                                                                                                                                                                                                                                                                                                               VIK D.P., MUNOZ-CANOVES P., KOZONO H., MARTIN L.G., TACK B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 WIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSY-WDYL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYKCDNGFSPPS-GYSWDYL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHKSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
 413
                            134
                                                         353
                                                                                                                 293 ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                 14 LTAWLSTAKGEVKSCEFFQFKYGRLYFEEILRPNFPVSIGNKYSYKCDNGFSPPSGLFWD 73
                                                                          74 YLRCTVQGWKPEVPCVRKCVFHYVENGEFAYWEKIYVQGQSLKVQCYNGYSLQNGQDTMT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RCTAQGWEPEVPCVRKCVFHYVENGDSTYWEKIYVQGQSLKVQCYNGYSLQNGQDTMTCT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGWSPPPKCIRIN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCT
                  CTENGWSPPPKCIRIK 149
 CTENGWSPPPKCVRIK 428
                                                        YLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYY 412
                                                                                                                                                                                                                                M29009; AAA37416.1; -. P08603; 1HCC. PF00084; sushi; 13. NCE 808 AA; 91654 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 33.5%;
Similarity 70.6%;
137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                        Similarity
90; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                         Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                        23.4%;
ilarity 66.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.70e-
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1129;
                                                                                                                                                                        24;
                                                                                                                                                                                      Score 790; DB 11;
Pred. No. 4.80e-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                   23644778 CRC32;
                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             808 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.70e-265;
atches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
                                                                                                                                                                           22;
                                                                                                                                                                                                       Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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RESULT RESULT OF A COMMENT OF A
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RR ROCC OSE DIT
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Best Local :
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091275
091275;
01-NOV-1996 (TIEMBLTel. 01, Created)
01-NOV-1996 (TIEMBLTel. 01, Last sequence update)
01-NOV-1996 (TIEMBLTel. 12, Last annotation update)
01-NOV-1996 (TIEMBLTel. 12, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
PATALABRAY REGULATORY PLASMA PROTEIN.
PATALABRAY REGULATORY (DATRED SAND DASS).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii.
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Percoidei; Serranidae; Paralabrax.
                                                                                                                       O08569 PRELIMINARY; PRT; 533 AA.

O08569; O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ACROSOMAL MATRIX COMPONENT AM67 PRECURSOR.
Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L21703; AAA92556.1;
HSSP; P08603; 1HFH.
PFAM; PF00084; Sushi; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neblifer).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement-regulatory plasma protein from barred sand bass (Parablax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAHMEN A., KAIDOH T., ZIPFEL P.F., GIGLI I.; "Cloning and characterization of a cDNA representing a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 94318039.
STRAIN-HARTLEY;
                               SEQUENCE FROM N.A.
                                                                                           Eutheria; Rodentia; Hystricognathi; Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 NDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQVIGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 AEPDQEYYFGQVVRFECNSGFKI-EGQKEMHCSENGLWSNEKPQCVEISCLPPRVENGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 HYVEYGESSYWQRR-YIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 ENIQDAVIVGTDKQIYNLNQKAIYACGEG-N--RGRITLTCGENGWSGDRKCT-VK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 YPGGRQVRVGCNVGY-S-GFFKLVCVEGKW-ETRGAK-CQPRSCGHPGDAQFADFHLAEG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWINDIPICEVVKCLPVTELENGRIVSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDSWDVRSWERY---TLDDNTRYWCKRGYKRTGGVTWA--TCGRNGWMPNPLCEVKTCSK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TP-HRIKHRIDDEIRYEC-KNGFYPATR-SPV-SKCTITG-WIPAPRCSLKPCDFPQFKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGAIREYKENDVLHYECDRAFKHIDRPSTCIKQGIKAEWSPTPLCESIKCRLTIMDGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PEEAT-FGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIENGNV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPC-LRQCIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYLKPVYKENERFQYKCKQGFVYKERGDA-VCTG--SGWNPQPSCEEMTCLTPYIPNGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPAYRNLFSPGETLKVICARTSWISTPQETSVVTTCQDNGEWSIRPTCQEVRCSNRRPEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132;
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Similarity 31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1053 AA;
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TISSUE-TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117597 MW; ODF68EDB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 683; DB 13; I
Pred. No. 2.44e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                     Q28769;
01-NOV-1996 (TIEMBLIET 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
COMPLEMENT RECEPTOR FRAGMENT).
                                                                             TISSUE-BONE MARROW;
BIRMINGHAM D.J., LOGAR C.M., SHEN X.P., CHEN W
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
                                                EMBL; L77977; AAA99004.1; -. HSSP; P08603; 1HFI.
                                                                                                                                                                                        Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
     SEQUENÇE
                      NON_TER
                                     PFAM;
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                   Papio.
                                                                                                                                                                            Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                Q28769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 97284752.

PROSTER J.A., FRIDAY B.B., MAULIT M.T., BLOBEL C., WINFREY V.P., OLSON G.E., KIM K.S., GERTON G.L.;

PAM67, a secretory component of the guinea pig sperm acrosomal matrix, is related to mouse sperm protein sp56 and the complement component 4-binding proteins.*;

J. Biol. Chem. 272:12714-12722(1997).

EMBL; U75654; AAC13888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         394 AKVQCHSGYSLPNGQDTYYCTEN-GWSPP-PKC 424
                                                                                                                                                                                                                                                                                                                                                                                                          434 VTIHCDSGYEVVGPQNII-CSENRTWTPEIPKC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00084; sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 DC-GPPPILPFASPVIQSY-ETNFRTGTALKYNCHRGYWRVNSSHVICDINGSWI-YN-V 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DCKGPPPREN-SEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCK-NGEWVPSNPS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YMCDEGYYPISADGRS--SCQADGMWNPKMPACESAVCLKPDILNGKLSVEKDHYTETEN 433
                                PF00084; sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Y-CDNGFTTPSQSYWDYLRCTVNG-WEPEVP-CLRQ-CIFHYVEYGESSYWQRRYIEGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATRSPVS-KCTIT-GWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPI-G-KEYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTPNEPRTVTCQENLKWAISKGCERVCCPTPNMEKMRII-NE-RRDPTGVCVYAYEDYIF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVC-TGSGWNPQ-PSCEEMTC--LT--PYIP-N-GIYT-PHRIKHRIDDEIRYECKNGFY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHCEANSKWYPSIPTCEPNGCIDLPEVPYISWERNVLSLKNQEIFEIGSLLKYDCKTGYR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SEN--GLWSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VANKTYGVWSSNPPTCEKVICROPHIPKGIFLSGFGFYYTYKDTLVISCKKGYILRGSSI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSDPLPECVIVKCDSPPDISNGK-HSGTDE-DL-YTYGSLVTYVCDPNYSLLGNASISCL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADG---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHC- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FCAKKRCRNPGELANG--KVEIITDLLFGSTIEFSCSKGYSLIGSTT-SQCESQGKTVD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .ch 15.4%; Score 520; DB 11; Length 533; Ll Similarity 27.2%; Pred. No. 3.02e-101; 123; Conservative 105; Mismatches 179; Indels 46;
52,2_AA;
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 AA;
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   56626 MW;
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7862072C CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOHI N., SAKÜRADA C., NONAKA M., OKADA N., OKADA H.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. EMBL; 136532; AAA91821.1; -. EMBL; D42115; BAA22548.1; -. HSSP; P10998; 1VVC. HSSP; P10998; 1VVC. PFAM; PF00084; Sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 96006570.
QUIGG R.J., LO C.F., ALEXANDER J.J., SNEED A.E., MOXLEY G. III;
"Molecular characterization of rat Crry: widespread distribution
"mo alternative forms of Crry mrna.";
Immunogenetics 42:362-367(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q63135;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat)
COMPLEMENT REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
151 AEAPICESIPCEIPPSIPNGDFFS--PNRE-DFHYGMVVTYQCNTDARGKKLFNLVGEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                    37 QCPAPPLFPYAKPINPT-DESTFPVGTSLKYECRPGYIKRQFSIT-CEVNSVWT-S-PQD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 PRCSLKPCD-F-PQFKHGRLYY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 CEEMTCLTP-YIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIP-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 PICTVKSCDDFLGQLPHGRVLF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 CSRV-COPPPEILHGEHTPSHODFSPGQEVFYSCEPG-Y-DLRGAASLHCTPQGDWNPEA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 VEIS-CLPPRVENGDGIYL-KPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 IIPNKCMPPNVENGVLVSVNRSLFSLNEVVEFRCQPGFVMKGPRHVQCQALNKWEPELPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 FPVGTYLKYECLPGYHG-KPFSIICLKNSVWTSAK-DK-CTRKSCRNPKD-PVNGM-VHV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.28;
Local Similarity 33.2%;
nes 107; Conservation
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                                                                  ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEID--YRECDAD-GWT 117
                                                                                                                                  VCIRKQCETPLDPQNG-I-VHVNTDIRFGSSITYTCNEGYRLIGSSSAMCIISDQSVAWD 150
                                                                                                                                                                                                        DCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCK-NGEWVPSNPSR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKDIQFGSQINYSCNKGYRLIGSSSATCIISGNTVIWDNETPICEIIPCGLPPT-IANGD
                                                                                                                                                                                                                                                                                                                                                                                    14.0%;
Similarity 26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 AA;
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                                                                                                                                                                                                                                                                                                                                              Conservative 114; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61680 MW; C87EEC58 CRC32;
                                                                                                                                                                                                                                                                                                                                                                             Score 471; DB 11;
Pred. No. 1.66e-88;
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Pred. No. 7.77e-91;
74; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 559;
                                                                                                                                                                                                                                                                                                                                          Indels 50;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DAY A.J., RIPOCHE J., LYONS A., MCINTOSH B., HARRIS T.J., SIM R.B.
"Sequence analysis of a CDNA clone encoding the C-terminal end of
human complement factor H.";
Biosci. Rep. 7:201-207(1987).
EMBL; M17517; AAA52016.1; -.
HSSP; P08603; hIFH.
HFH.
HFS.P. P08603; HIFH.
HFS.P. P08603; Sushi: 11.
      486
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                                   261
                                                                428
                                                                                                                             368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326
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                                                                                                                                                                                                                                                                                                                                                              Local
VSRQMSKYP-S-GERVRYQCRSPYEMFGDE--EVM-CLNGNWTEPPQCKDSTGKCGPPPP
                                                                                                                   VAHMSDSYQYGEEVTYKCFEGFGIDGPAIAKCLGEKWSHPPSCIKTDCLSLPSFENAIPM
                                                                                                                                                                                                                                             LNYRDGEKVSVLCQENY-LIQEGEEITCKDGRW-QSIPLCVEKIPCSQPPQIEHGTINSS 310
                                                                                                                                                                                                                                                                             YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG
                             PHRIK-HRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAPRCSLKPCDFPQFKHGRLYY 319
                                                          GEKKDVYKAGEQVTYTC-ATYYKMDGASNVTCINSRWTGRPTCRDTSCVNPPTVQNA-YI
                                                                                         GIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLT-PYIPNGIYT
                                                                                                                                                     AAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCL-PPRVENGD
                                                                                                                                                                                  RS-SQESYAHGTKLSYTCEGGFRISEENETTCY-MGKWSSP-PQCEGLPCKSPPEISHGV 367
                                                                                                                                                                                                                   SEFEFGAKVVYTCDEGYOLLGEIDYRECDADGWTNDIPIC~EVVKCLPVTELENGRIVSG
                                                                                                                                                                                                                                                                                                            FDHNSNIRYRCR-G-KE-GWIHTVCINGRWDPEVNCSMAQIQLCPPPPQIP-NSHNMTTT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNS---G---FKIEGQKE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VALECEDGYTLEGSSQSQC-QSDAS-WDPPLPKCVSQVICKLPQDMSGFQKGLQMKKDYY 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYPATRSPVSKCTITG----WIPA-PRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHCTSIDGQVGVWSGPPPQCIELNKCTPPHVENAVIVSKNKSLFSLRDMVEFRCQDGFMM 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGDNVALECEDGYTLEGSSQSQCQSDASWDPPLPKCV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVP-CLRQ--CIFHYVEYG-ESSYWQRR-YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KERGDAVCTG-SGWNPQ-PSC-EEMTC--LTPYIPNG-IYTPHRIKHRIDDEIRYECKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGDSSVYCRSLNRWEPQLPSCFKVKSCGAFLGELPNGHVFVPQNL-Q-LGAKVTFVCNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHC-S-EN--GLWSNEKPQCVEIS-CLPPRVENGDGIYL-KPVYKENERFQYKCKQGFVY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -YQLKGNSSSHCVLDGVESIWNSSVPVCEQVICKLPQDMSGFQKGLQMKKDYY---YGDN 381
                                                                                                                                                                                                                                                                                                                                                             h 13.9%;
Similarity 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          657 AA; 74247 MW;
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                             Score 470; DB 4;
Pred. No. 3.02e-88;
                                                                                                                                                                                                                                                                                                                                                                                                          F4AB5238 CRC32;
                                                                                                                                                                                                                                                                                                                                            Mismatches 201; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                          Length 657;
                                                                                                                                                       201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 90229754.

KURTZ C.B., O'TOOLE E., CHRISTENSEN S.M., WEIS J.H.;

KURTZ C.B., O'TOOLE E., CHRISTENSEN S.M., WEIS J.H.;

"The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cofactor protein.";
J. Exp. Med. 181:151-159(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mouse complement regulatory protein Crry/p65 uses the mechanisms of both human decay-accelerating factor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 21-367 FROM N.A.
MEDLINE; 95105691.
MIN Y.U., KINOSHITA T., MOLINA H., HOURCADE D., SEYA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q99254
Q99254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement pathway; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING OF CR2 GENE TRANSCRIPTS PREDICTS TWO DISTINCT GENE PRODUCTS THAT SHARE HOMOLOGOUS DOMAINS WITH BOTH HUMAN CR2 AND CR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOLERS V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
-!- TISSUE SPECIFICITY: B LYMPHOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALTERNATIVELY SPLICED VERSION) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH BOTH EXECUTION IN THE STATE OF THE STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 IDNGDITSFPLSVYAPASSVEYQCQNLYQL-EGNKRITCRNGQWSEPPKCLH 591
                                                                                                                                83
                                                                                                                                                                                                                                                                        24 YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
                                                                                                                                                                                                                                                                                                                                                 42 FAIGTTWEYKCRPGYFRKSFIIT-CLETSKW---SDAQQFCKRKPCMNPQEPLHGSVHINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunol. 144:3581-3591(1990).
                                                                                                                    GSEFEFGAKVVYTCDEGYQLLGE--IDYRECDADG-WTNDIPICEVVKCLPVTELENGRI
                                                                                                                                                                                            G--IEFGSTITYSCNQGYRLIGDSSATCIVSDNTVMWDNDMPLCESIPCESPPAISNGDF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:88489; Cr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGW-EP-EV-PCLRQC-IFHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00084; sushi; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P10998; 1VVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     679
74916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.9%;
31.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 470; DB 11;
Pred. No. 3.02e-88;
72; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENT RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF08AC75
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
                                                                                                                        139
                                            213
                                                                                                                                                                                                                                                                                                                                                     98
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RESULT RE
RESULT 13
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Best Local (
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PRELIMINARY; PRT; 1911 AA.
O29528;
O1-NOV-1996 (TIEMBLIFE). 01, Created)
O1-NOV-1999 (TIEMBLIFE). 12, Last sequence update)
O1-NOV-1999 (TIEMBLIFE). 12, Last annotation update)
COMPLEMENT RECEPTOR 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases EMBL; L39791; AAA62170.1; -. HSSP; P08603; IHCC. HSSP; P08603; LHCC. PFAM: PF00084; sushi; 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEMENZA L., SUBRAMANIAN B.V., NICKELLS M.W., ATKINSON J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         1193 RSLWNNSVPVC 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             850 FPIGTSLKYECRPEYYG-KPFSITCLD-NLVWSSPKDVCKRKSCKTPPD-PVNGM-VHVI 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 13.5%;
Local Similarity 31.8%;
hes 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEVKSCDAIPNHLLHGRVF 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F-MGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPG-YTLIGTNLVECTSLGTWSNTVPT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ISCLPPRVENG--DGIYLKPVYKENERFQYKCKQGFVYKERGDAVC-TGSGWNPQ-PSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSGAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHC-S-EN--GLWSNEKPQCVE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEMTCLTP-YIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG-WIPA-PR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVKCPMPEIENGLVESGF-KHSFFLNDTVIFKCKSGFTMKGSRIAWCQPNSKWSPPLPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEIS-CLPPRVENGDGIYL-KPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 178GAAEPDQEYY-FGQVVRFECN--SGFK-I-E--GQKEMHC-S-EN--GLWSNEKPQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEFEFGAKVVYTCDEGYQLLGEIDYREC--DAD-G-WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDIQVGSRINYSCTTGHRLIGHSS-AECIISGNTAHWSTKPPICQRIPCGLP-PPIANGD 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG
                                                                                                                                                              NG-WEPEVP-C
                                                                                                                                                                                                                                                                                                                     APRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTV 358
                                                                                                                                                                                                                                                                                                                                                                                            APRCAVKSCD--DF-LGQLHHGRVLVP-FNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGM 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEEMTCLTP-YIPNGIYTP-HRIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSRV-CQPPPEILHGEHTPSHQDKFSPGQEVFYSCEPG-Y-DLRGAASLHCTPQGDWSPE 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIPNKCMPPNVENGILVSVNRSLFSLNEVVEFRCQPGFVMKGPRRVQCQALNKWEPELPS 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIS--T--NREYFHYGSVVTYRCNLGSGRKKLFELVGEPSIYCTSKDDQVGIWSGPAPQC 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1911 19
1911 AA;
PRELIMINARY;
                                                                                                                                                                  367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210173 MW; 03D640C2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 456; DB 6; Length 1911; Pred. No. 1.25e-84; 81; Mismatches 128; Indels 44;
               331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOURCADE D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
δÃ
                                                             DЬ
                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                         Query Match 13.3%;
Best Local Similarity 41.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                             Matches
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01-FEB-1997 (TIEMBLIEL. 02, Created)
01-FEB-1997 (TIEMBLIEL. 02, Last sequence update
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update
COMPLEMENT EACTOR H-RELATED PROTEIN 4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q61406 PRELIMINARY; PRT; Q61406; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1999 (TrEMBLrel. 12, Last ann 01-NOV-1999 (TrEMBLrel. 12, Last ann 01-NOV-1999 (TrEMBLrel. 12)
                                                                                                                                                                                                                                                                                                                  VIK D.P., MUNOZ-CANOVES P., KOZONO H., MARTIN L.G., TACK B.F., CHAPLIN D.D.;
"Identification and sequence analysis of four complement factor related transcripts in mouse liver.";
related transcripts in mouse liver.";
Biol. Chem. 265:3193-3201(1990).
EMBL; M29008; AAA37414.1; -.
HSSP; P08603; 1HFI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                       FRAM; PF00084; sushi; 4.

SECUTION SECU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 90153969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENT FACTOR H-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X98337; CAA66980.1; HSSP; P10998; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat-containing protein is associated lipoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 T--YYCTENGWSPPPKCVRI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 SGSITCLQNGWSAQPICIKF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 DYLRCTVNGWEPEVPCLRQCI-FHY-VEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 ITGWIPAPRC-SLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYW 351
293 ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 13.3%;
Local Similarity 43.6%;
hes 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 DYIHCTQDGWLPTVPCLRTCSKSDIEIENGFISESSSIYILNKEIQYKCKPGYATADGNS 128
                                                             14 LTSWFSTAKGEVSLCDFPKIRHGILYDEKKNEPFSSVLSGKILYYSCEYNFASPSNSFWT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LILWYSCANGQEYKPCDFPEIQHGGLYYKSLRRLYFPAAAGQSYSYYCDQNFYTPSGSYW 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00084; sushi; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
331 AA;
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272:5627-5634(1997).
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37325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 448; DB 4;
Pred. No. 1.44e-82;
22; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                         Score 447; DB 11;
Pred. No. 2.60e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                          29; Mismatches 49;
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COMPLEMENT FACTOR H-RELATED PROTEIN 4.; 2505D66C CRC32;
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                                                                                                                                                                                           Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.3%;
Best Local Similarity 32.3%;
Matches 104; Conservative
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SEQUENCE
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029531; O1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COMPLEMENT RECEPTOR 1 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L24921; AAA51439.1; -. HSSP; P10998; IVVC. PFAM; PF00084; sushi; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIRMINGHAM D.J., SHEN X.P., HOURCADE D., NICKELLS M.W., ATKINSON J.P., "Primary sequence of an alternatively spliced form of CR1. Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee erythrocytes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 94292799.
                                                                                                                                                                                                                                     189 EIS-CLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                     139
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                                                                                                                                                                                                                                                                                             209 IPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCOPGFVMKGPPRVKCOALNKWEPELPSC 268
                                                                                                                                                                                                                                                                                                                                                                                                              152 FIS--THRE-NEHYGSVYTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|:||| |||:
413 CTENGWSPPPKCV 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSEFEFGAKVVTCDEGYQLLGEIDYR-ECDADG--WINDIPICEVVKC-LPVTELENGR 138
                                                                                                                    EEMTCLTP-YIPNGIYTPH-RIKHRIDDEIRYECKNGFYPATRSPVS-KCTITG-WIPA-
                                                                                                                                                                                                                                                                                                                                                         IKDIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSEGTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAV 82
PRCSLKPCD-F-PQFKHGRLYY 319
                                                           PTCEVKSCDDFMGQLLNGRVLF 347
                                                                                                                                                                         SRV-CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG-Y-DLRGAASLRCTPQGDWSPAT 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153:691-700(1994).
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>661 COMPLEMENT RECEPTO
661
4; 72966 MW; 9D78E262 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 449; DB 6; Length 661; Pred. No. 7.94e-83; 73; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENT RECEPTOR 1.
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                                                                                                                    299
                                                                                                                                                                                                                                     244
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Search completed: Thu Jun -8 21:51:46 2000 Job time : 40 secs.